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OM protein - protein search, using sw model

Run on: October 13, 2005, 18:47:27 ; Search time 23 Seconds  
(without alignments)  
707.543 Million cell updates/sec

Title: US-10-694-978-4

Perfect score: 218

Sequence: 1 MSFVGNSGVKMGSEWEDK.....IEFSQPVCKAEMSPSEVSD 218

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 6

Total number of hits satisfying chosen parameters: 652

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	129	59.2	178	3	US-09-128-155-2
6	115	52.8	115	3	US-09-128-155-5
7	115	52.8	115	3	US-09-128-155-9
8	115	52.8	115	3	US-09-128-155-13
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12	19	8.7	52	3	US-09-128-155-8
13	14	6.4	21	3	US-09-128-155-12
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27	7	3.2	264	4	US-09-107-532A-7009

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255	6	2.8	280	4	US-10-101-464A-621	Sequence 461, App	328	6	385	4	US-09-270-767-32506	Sequence 32506, A
256	6	2.8	281	4	US-09-134-000C-4462	Sequence 4462, Ap	329	6	385	4	US-09-270-767-47723	Sequence 47723, A
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260	6	2.8	300	4	US-09-949-016-10794	Sequence 10794, A	333	6	399	4	US-09-222-938A-49	Sequence 49, Appl
261	6	2.8	304	4	US-09-252-991A-22398	Sequence 22398, A	334	6	400	4	US-09-949-016-7917	Sequence 7917, Ap
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263	6	2.8	307	4	US-09-454-071-3	Sequence 3, Appl	336	6	407	4	US-09-543-681A-7929	Sequence 7929, Ap
264	6	2.8	308	4	US-08-311-731A-148	Sequence 148, App	337	6	409	4	US-09-949-016-11637	Sequence 11637, A
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267	6	2.8	310	4	US-09-524-730-2	Sequence 2, Appl	340	6	413	4	US-09-248-796A-18656	Sequence 18656, A
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274	6	2.8	312	4	US-09-248-796A-16990	Sequence 16990, A	347	6	424	4	US-09-252-991A-3212	Sequence 3212, A
275	6	2.8	314	4	US-09-544-618-20	Sequence 20, Appl	348	6	429	1	US-07-672-483-3	Sequence 3, Appl
276	6	2.8	314	4	US-09-902-540-10595	Sequence 10595, A	349	6	429	3	US-09-370-368-6	Sequence 6, Appl
277	6	2.8	317	4	US-09-270-767-46456	Sequence 46456, A	350	6	429	6	5182195-13	Patent No. 5182195
278	6	2.8	320	4	US-09-270-767-44175	Sequence 44175, A	351	6	429	6	5182195-13	Patent No. 5182195
279	6	2.8	321	4	US-09-795-926-35	Sequence 35, Appl	352	6	431	4	US-09-328-352-7392	Sequence 7392, Ap
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281	6	2.8	324	4	US-09-328-352-4636	Sequence 4636, Ap	354	6	433	3	US-08-941-532-6	Sequence 6, Appl
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284	6	2.8	332	4	US-09-602-777A-308	Sequence 308, App	357	6	433	4	US-10-151-668-2	Sequence 2, Appl
285	6	2.8	333	4	US-09-538-092-778	Sequence 778, App	358	6	434	2	US-08-487-113D-120	Sequence 120, App
286	6	2.8	334	3	US-09-120-365-64	Sequence 64, Appl	359	6	434	2	US-08-720-420A-120	Sequence 120, App
287	6	2.8	334	3	US-09-515-039-64	Sequence 64, Appl	360	6	434	4	US-09-270-767-41796	Sequence 41796, A
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296	6	2.8	346	2	US-08-459-448A-19	Sequence 19, Appl	369	6	443	3	US-08-993-359-30	Sequence 30, Appl
297	6	2.8	346	3	US-08-459-595A-19	Sequence 19, Appl	370	6	443	4	US-09-273-871A-5	Sequence 5, Appl
298	6	2.8	346	3	US-08-459-504B-19	Sequence 19, Appl	371	6	443	4	US-09-482-558A-30	Sequence 30, Appl
299	6	2.8	346	3	US-08-459-444-19	Sequence 19, Appl	372	6	443	4	US-10-083-452-5	Sequence 5, Appl
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319	6	2.8	377	3	US-09-239-843A-42	Sequence 42, Appl	392	6	464	3	US-08-802-805D-6	Sequence 6, Appl

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395	6	2.8	464	4	US-09-388-116C-6	Sequence 6, Appli	468	6	2.8	637	4	US-09-390-224-4	Sequence 4, Appli
396	6	2.8	470	4	US-09-291-299A-1	Sequence 1, Appli	469	6	2.8	640	4	US-09-328-352-8058	Sequence 8058, Ap
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398	6	2.8	476	4	US-09-733-524A-5	Sequence 5, Appli	471	6	2.8	643	4	US-09-949-016-10893	Sequence 10903, A
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414	6	2.8	508	4	US-08-781-986A-5241	Sequence 5241, Ap	487	6	2.8	716	3	US-08-818-823-4	Sequence 4, Appli
415	6	2.8	510	3	US-09-134-001C-4541	Sequence 4541, Ap	488	6	2.8	716	3	US-09-037-190-38	Sequence 38, Appl
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439	6	2.8	556	4	US-09-438-185A-210	Sequence 210, App	512	6	2.8	739	4	US-10-202-619-2	Sequence 2, Appli
440	6	2.8	558	4	US-09-540-236-2943	Sequence 2943, Ap	513	6	2.8	744	4	US-09-328-352-7920	Sequence 7920, Ap
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446	6	2.8	577	4	US-09-248-796A-18822	Sequence 18822, A	519	6	2.8	762	2	US-08-907-166-10	Sequence 10, Appl
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448	6	2.8	580	4	US-09-123-668-1	Sequence 1, Appli	521	6	2.8	762	4	US-09-724-653-7	Sequence 7, Appli
449	6	2.8	582	3	US-08-906-865-3	Sequence 3, Appli	522	6	2.8	764	4	US-09-370-838-67	Sequence 67, Appl
450	6	2.8	582	4	US-09-129-668-3	Sequence 3, Appli	523	6	2.8	764	4	US-09-538-092-944	Sequence 944, App
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453	6	2.8	591	4	US-09-688-188B-103	Sequence 103, App	526	6	2.8	766	4	US-09-724-653-14	Sequence 14, Appl
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455	6	2.8	591	4	US-09-291-417D-103	Sequence 103, App	528	6	2.8	772	3	US-09-134-078-28	Sequence 28, Appl
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542	6	2.8	812	4	US-09-949-016-6694	Sequence 6694, Ap	615	2.8	1984	4	US-09-949-016-7111	Sequence 7111, Ap
543	6	2.8	816	2	US-08-533-306A-6	Sequence 6, Appli	616	2.8	1984	4	US-09-949-016-7112	Sequence 7112, Ap
544	6	2.8	816	2	US-08-742-923A-6	Sequence 6, Appli	617	2.8	1984	4	US-09-949-016-7113	Sequence 7113, Ap
545	6	2.8	816	2	US-09-540-236-3443	Sequence 3443, Ap	618	2.8	2109	3	US-08-646-695-6	Sequence 6, Appli
546	6	2.8	820	1	US-08-291-896-2	Sequence 2, Appli	619	2.8	2109	5	PCT-US96-06053-6	Sequence 6, Appli
547	6	2.8	820	2	US-08-485-278-2	Sequence 2, Appli	620	2.8	2201	4	US-09-539-601-6	Sequence 6, Appli
548	6	2.8	823	4	US-09-949-016-6852	Sequence 6852, Ap	621	2.8	2201	4	US-09-539-601-15	Sequence 15, Appli
549	6	2.8	824	4	US-09-134-000C-4908	Sequence 4908, Ap	622	2.8	2201	4	US-10-029-907-3	Sequence 3, Appli
550	6	2.8	830	4	US-09-107-532A-5709	Sequence 5709, Ap	623	2.8	2321	4	US-09-230-652-2	Sequence 2, Appli
551	6	2.8	833	4	US-09-252-991A-25227	Sequence 25227, A	624	2.8	2472	4	US-09-538-092-1312	Sequence 1312, Ap
552	6	2.8	834	4	US-09-949-016-10381	Sequence 10381, A	625	2.8	2595	3	US-09-036-987A-2	Sequence 2, Appli
553	6	2.8	853	1	US-08-638-911A-25	Sequence 25, Appli	626	2.8	2595	3	US-09-370-700-2	Sequence 2, Appli
554	6	2.8	853	1	US-08-638-911A-27	Sequence 27, Appli	627	2.8	2595	4	US-09-603-207-2	Sequence 2, Appli
555	6	2.8	853	1	US-08-638-911A-29	Sequence 29, Appli	628	2.8	2842	1	US-07-741-940-7	Sequence 7, Appli
556	6	2.8	853	1	US-08-638-911A-31	Sequence 31, Appli	629	2.8	2842	1	US-08-289-548A-7	Sequence 7, Appli
557	6	2.8	859	4	US-09-538-092-206	Sequence 206, App	630	2.8	2842	1	US-08-452-654-7	Sequence 7, Appli
558	6	2.8	869	4	US-09-252-991A-22290	Sequence 22290, A	631	2.8	2842	4	US-08-449-731-7	Sequence 7, Appli
559	6	2.8	869	4	US-09-949-016-11193	Sequence 11193, A	632	2.8	2843	1	US-07-741-940-2	Sequence 2, Appli
560	6	2.8	874	4	US-09-187-330-59	Sequence 59, Appli	633	2.8	2843	1	US-08-289-548A-2	Sequence 2, Appli
561	6	2.8	881	4	US-09-248-796A-18627	Sequence 18627, A	634	2.8	2843	1	US-08-452-654-2	Sequence 2, Appli
562	6	2.8	885	2	US-08-533-306A-4	Sequence 4, Appli	635	2.8	2843	1	US-08-452-655B-2	Sequence 2, Appli
563	6	2.8	885	2	US-08-742-923A-4	Sequence 4, Appli	636	2.8	2843	1	US-08-452-655B-7	Sequence 7, Appli
564	6	2.8	919	4	US-09-248-796A-17485	Sequence 17485, A	637	2.8	2843	3	US-08-370-235A-2	Sequence 2, Appli
565	6	2.8	921	4	US-09-699-266A-9	Sequence 9, Appli	638	2.8	2843	3	US-08-450-582-2	Sequence 2, Appli
566	6	2.8	931	4	US-09-079-592-11	Sequence 11, Appli	639	2.8	2843	3	US-08-450-582-7	Sequence 7, Appli
567	6	2.8	934	4	US-09-949-016-7286	Sequence 7286, Ap	640	2.8	2843	4	US-08-449-731-2	Sequence 2, Appli
568	6	2.8	942	4	US-09-254-776B-51	Sequence 51, Appli	641	2.8	2843	4	US-10-092-138A-30	Sequence 30, Appli
569	6	2.8	981	4	US-09-252-991A-24231	Sequence 24231, A	642	2.8	2843	4	US-09-538-092-1007	Sequence 1007, Ap
570	6	2.8	989	4	US-09-248-796A-19109	Sequence 19109, A	643	2.8	2973	2	US-08-821-355A-7	Sequence 7, Appli
571	6	2.8	998	4	US-09-949-016-7757	Sequence 7757, Ap	644	2.8	2973	2	US-09-003-687A-7	Sequence 7, Appli
572	6	2.8	1000	4	US-09-187-330-1	Sequence 1, Appli	645	2.8	2973	3	US-09-136-605-7	Sequence 7, Appli
573	6	2.8	1076	4	US-09-949-016-6610	Sequence 6610, Ap	646	2.8	3010	4	US-09-539-601-3	Sequence 3, Appli
574	6	2.8	1077	4	US-09-412-210-1	Sequence 1, Appli	647	2.8	3010	4	US-09-539-601-21	Sequence 21, Appli
575	6	2.8	1077	4	US-10-121-911A-1	Sequence 1, Appli	648	2.8	3010	4	US-09-539-601-27	Sequence 27, Appli
576	6	2.8	1085	4	US-09-095-881-2	Sequence 2, Appli	649	2.8	3010	4	US-09-539-601-33	Sequence 33, Appli
577	6	2.8	1089	4	US-09-248-796A-19072	Sequence 19072, A	650	2.8	3169	3	US-09-453-702B-257	Sequence 257, App
578	6	2.8	1095	4	US-09-555-554-4	Sequence 4, Appli	651	2.8	3913	4	US-09-949-016-10933	Sequence 10933, A
579	6	2.8	1100	4	US-09-949-016-7524	Sequence 7524, Ap	652	2.8	4377	4	US-09-949-016-6978	Sequence 6978, Ap
580	6	2.8	1102	4	US-09-364-609-8	Sequence 8, Appli						
581	6	2.8	1113	4	US-09-332-522E-2	Sequence 2, Appli						
582	6	2.8	1116	4	US-09-252-991A-32442	Sequence 32442, A						
583	6	2.8	1130	4	US-09-538-092-834	Sequence 834, App						
584	6	2.8	1140	2	US-08-657-641-7	Sequence 7, Appli						
585	6	2.8	1140	5	PCT-US94-07233-7	Sequence 7, Appli						
586	6	2.8	1148	4	US-09-949-016-6798	Sequence 6798, Ap						
587	6	2.8	1164	4	US-09-949-016-9269	Sequence 9269, Ap						
588	6	2.8	1169	4	US-09-949-016-9630	Sequence 9630, Ap						
589	6	2.8	1192	4	US-09-902-540-12662	Sequence 12662, A						
590	6	2.8	1203	3	US-09-351-200-2	Sequence 2, Appli						
591	6	2.8	1217	4	US-09-949-016-7454	Sequence 7454, Ap						
592	6	2.8	1237	1	US-08-241-853-2	Sequence 2, Appli						
593	6	2.8	1237	2	US-08-850-917-2	Sequence 2, Appli						
594	6	2.8	1278	4	US-09-902-540-16646	Sequence 16646, A						
595	6	2.8	1289	4	US-09-949-016-7313	Sequence 7313, Ap						
596	6	2.8	1342	4	US-09-561-709B-13	Sequence 13, Appli						
597	6	2.8	1427	4	US-09-538-092-1044	Sequence 1044, Ap						
598	6	2.8	1463	4	US-09-949-016-11696	Sequence 11696, A						
599	6	2.8	1464	3	US-08-891-640-2	Sequence 2, Appli						
600	6	2.8	1464	4	US-09-949-016-6738	Sequence 6738, Ap						
601	6	2.8	1564	4	US-09-976-594-309	Sequence 309, App						
602	6	2.8	1596	4	US-09-538-092-887	Sequence 887, App						
603	6	2.8	1621	3	US-08-972-927-3	Sequence 3, Appli						
604	6	2.8	1622	4	US-09-231-899-72	Sequence 72, Appli						
605	6	2.8	1665	4	US-09-858-664A-2	Sequence 2, Appli						
606	6	2.8	1665	4	US-10-274-978-2	Sequence 2, Appli						
607	6	2.8	1665	4	US-10-657-263-2	Sequence 2, Appli						
608	6	2.8	1724	4	US-09-607-510-2	Sequence 2, Appli						
609	6	2.8	1857	4	US-09-917-254-91	Sequence 91, Appli						
610	6	2.8	1938	4	US-09-949-016-6417	Sequence 6417, Ap						
611	6	2.8	1959	4	US-09-949-016-8134	Sequence 8134, Ap						

## ALIGNMENTS

## RESULT 1

US-09-398-412B-4  
; Sequence 4, Application US/09398412B  
; Patent NO. 6680380

; GENERAL INFORMATION:  
; APPLICANT: Titanas, Jacqueline C.  
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-lzeta, related reage

; FILE REFERENCE: DX0904K  
; CURRENT APPLICATION NUMBER: US/09/398.412B

; CURRENT FILING DATE: 1999-09-17  
; PRIOR FILING DATE: 1998-09-18

; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4  
; LENGTH: 218

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-398-412B-4

Query Match 100.0%; Score 218; DB 4; Length 218;

Best Local Similarity 100.0%; Pred. NO. 1.5e-212; Indels 0; Gaps 0;

Matches 218; Conservative 0; Mismatches 0;

1 MSFVGENSGVKGSGEDWEKDEPQCCLEDPAVSPLEPGFSLPAMNFVHTSPKVNLPKPF 60

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Db      1  MSFVGENSGVKMGSEDEKDEPOCCLEDPVSPLEPGSLPAMNFVHTSPKVNLPKPF 60
Qy      61 SIHQDHKVLVLDSCNLIAPDKNIIRPEIFFALASSLSASAEGKSPILLGVSKGEFCL 120
      |||
Db      61 SIHQDHKVLVLDSCNLIAPDKNIIRPEIFFALASSLSASAEGKSPILLGVSKGEFCL 120
      |||
Qy      121 YCDKDKGQSHPSLQKKEKMLKLAQKESARRRPFIFYRAQVGSNNMLESAAHPGWFTCTS 180
      |||
Db      121 YCDKDKGQSHPSLQKKEKMLKLAQKESARRRPFIFYRAQVGSNNMLESAAHPGWFTCTS 180
      |||
Qy      181 CNCNEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD 218
      |||
Db      181 CNCNEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD 218
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* RESULT 2
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match      80.7%; Score 176; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.9e-170;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      43 MNFVHTSPKVNLPKPFSTHDQDHKVLVLDSCNLIAPDKNIIRPEIFFALASSLSAS 102
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Db      43 MNFVHTSPKVNLPKPFSTHDQDHKVLVLDSCNLIAPDKNIIRPEIFFALASSLSAS 102
      |||
Qy      103 AEKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQKESARRRPFIFYRAQV 162
      |||
Db      103 AEKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQKESARRRPFIFYRAQV 162
      |||
Qy      163 SNNMLESAAHPGWFTCTSCNCPNPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
      |||
Db      163 SNNMLESAAHPGWFTCTSCNCPNPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
      |||

RESULT 3
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

Query Match      59.2%; Score 129; DB 3; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e-122;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      90 IFFALASSLSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQKES 149
      |||
Db      39 IFFALASSLSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQKES 98
      |||
Qy      150 ARPPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCPNPVGVTDKFENRKHIEFSFQPVCKA 209
      |||
Db      99 ARPPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCPNPVGVTDKFENRKHIEFSFQPVCKA 158
      |||

RESULT 5
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

Query Match      59.2%; Score 129; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.4e-122;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      90 IFFALASSLSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQKES 149
      |||
Db      39 IFFALASSLSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQKES 98
      |||
Qy      150 ARPPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCPNPVGVTDKFENRKHIEFSFQPVCKA 209
      |||
Db      99 ARPPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCPNPVGVTDKFENRKHIEFSFQPVCKA 158
      |||
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

Query Match      59.2%; Score 129; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  90  IFFALASSLSASAEKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKES 149
Db  50  IFFALASSLSASAEKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKES 109

Qy  150  ARRPPIFYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKA 209
Db  110  ARRPPIFYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKA 169

Qy  210  EMSPSEVSD 218
Db  170  EMSPSEVSD 178

RESULT 6
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

Query Match      52.8%; Score 115; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  104  EKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 163
Db  1    EKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 60

Qy  164  WNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
Db  61  WNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 115

RESULT 7
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
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; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-9

Query Match      52.8%; Score 115; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  104  EKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 163
Db  1    EKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 60

Qy  164  WNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
Db  61  WNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 115

RESULT 8
US-09-128-155-13
; Sequence 13, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-13

Query Match      52.8%; Score 115; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  104  EKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 163
Db  1    EKGSPIILGVSKGEFCLYCDKDKGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 60

Qy  164  WNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218
Db  61  WNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 115

RESULT 9
US-09-398-412B-2
; Sequence 2, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
```



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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-2

Query Match      25.2%; Score 55; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILLGVSGECLYCDKDGSHPSLQIKKELMKLAQKESARRPFIFYRAQVGS 163
Db 109 ILLGVSGECLYCDKDGSHPSLQIKKELMKLAQKESARRPFIFYRAQVGS 163

RESULT 10
US-09-128-155-18
; Sequence 18, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: synthetically generated
; LOCATION: (1)...(185)
; OTHER INFORMATION: human sequence predicted using an alignment algorithm which
; OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
; OTHER INFORMATION: interest in a stretch of genomic DNA
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(185)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18

Query Match      23.9%; Score 52; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 KEKLMKLAQKESARRPFIFYRAQVGSNNMLESAAHPGWFICTSCNCPVVG 188
Db 113 KEKLMKLAQKESARRPFIFYRAQVGSNNMLESAAHPGWFICTSCNCPVVG 164

RESULT 11
US-09-128-155-4
; Sequence 4, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
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; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-4

Query Match      13.8%; Score 30; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 9.3e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFVGNSGVKMGSEDEWKEDEPOCCLEDDPA 30
Db 1 MSFVGNSGVKMGSEDEWKEDEPOCCLEDDPA 30

RESULT 12
US-09-128-155-8
; Sequence 8, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-8

Query Match      8.7%; Score 19; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MGSEDEWKEDEPOCCLEDDPA 30
Db 1 MGSEDEWKEDEPOCCLEDDPA 19

RESULT 13
US-09-128-155-12
; Sequence 12, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-12
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Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Search completed: October 13, 2005, 18:55:15  
Job time : 35 secs

Qy 90 IFFALASSLSASA 103  
| | | | | | | | | |  
Db 8 IFFALASSLSASA 21

RESULT 14  
US-09-364-206-47  
; Sequence 47, Application US/09364206  
; Patent No. 6475752  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Baugh, Mariah R.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: Mammalian Imidazoline Receptor  
; FILE REFERENCE: PC-0006 US  
; CURRENT APPLICATION NUMBER: US/09/364,206  
; CURRENT FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PERL Program  
; SEQ ID NO 47  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY:  
; OTHER INFORMATION: W43396  
; PUBLICATION INFORMATION:  
US-09-364-206-47

Query Match 3.7%; Score 8; DB 4; Length 559;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
| | | | | | | | | |  
Db 106 ALASSLS 113

RESULT 15  
US-08-650-766-6  
; Sequence 6, Application US/08650766D  
; Patent No. 6015690  
; GENERAL INFORMATION:  
; APPLICANT: PILETZ, John E.  
; APPLICANT: IVANOV, Tina R.  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND  
; TITLE OF INVENTION: METHOD FOR CLONING THE SAME  
; FILE REFERENCE: Corrected Sequence Listing  
; Patent No. 6015690  
; CURRENT APPLICATION NUMBER: US/08/650,766D  
; CURRENT FILING DATE: 1996-05-20  
; EARLIER APPLICATION NUMBER: US 60/012,600  
; EARLIER FILING DATE: 1996-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 651  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-650-766-6

Query Match 3.7%; Score 8; DB 3; Length 651;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
| | | | | | | | | |  
Db 106 ALASSLS 113

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2005, 18:50:57 ; Search time 176 Seconds  
(without alignments)  
634.280 Million cell updates/sec

Title: US-10-694-978-4

Perfect score: 218

Sequence: 1 MSFVGENSGVMGSEDWEK.....IEFSFQPVCKAEMSPSEVSD 218

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4696

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	55	25.2	219	1	Q7ru00 homo sapien
3	9	4.1	196	2	Q97cb6 thermoplasm
4	8	3.7	97	2	Q9SAQ1
5	8	3.7	161	2	Q8ZQJ2
6	8	3.7	234	2	Q87JK9
7	8	3.7	256	2	Q72ME6
8	8	3.7	256	2	Q8EY26
9	8	3.7	267	2	Q73909
10	8	3.7	341	1	LPSL RHIME
11	8	3.7	412	1	PDK4 MOUSE
12	8	3.7	413	2	Q9YCD8
13	8	3.7	595	2	Q9UEU4
14	8	3.7	787	2	Q8RX76
15	8	3.7	931	2	Q7SE30
16	8	3.7	982	2	Q65833
17	8	3.7	982	2	Q93Y88
18	8	3.7	993	2	Q7L8M3
19	8	3.7	1354	2	Q9EPW8
20	8	3.7	1427	1	ABCI SCHPO
21	8	3.7	1480	2	Q80TM9
22	8	3.7	1504	2	Q8FGP3
23	8	3.7	1504	2	Q6PIB4
24	8	3.7	1504	2	Q722X6
25	8	3.7	1504	2	Q9UEB6
26	8	3.7	1528	2	Q9Y211
27	8	3.7	1622	2	O24635
28	8	3.7	1622	2	Q9C8G9
29	8	3.7	2118	2	O76904
30	7	3.2	55	2	Q6QW36
31	7	3.2	73	2	Q8HXG7

32	7	3.2	88	2	Q8IGB4	Q81ge4 drosophila
33	7	3.2	89	2	Q8LC91	Q81c91 arabidopsis
34	7	3.2	91	2	Q86H93	Q86h93 dictyosteli
35	7	3.2	98	2	Q7Q5G1	Q7q5g1 anopheles g
36	7	3.2	99	2	Q6UXS1	Q6uxs1 homo sapien
37	7	3.2	107	2	Q9GYD7	Q9gyd7 leishmania
38	7	3.2	116	2	Q9YA88	Q9ya88 aeropyrum p
39	7	3.2	118	2	Q9MZQ7	Q9mzq7 lepus towns
40	7	3.2	118	2	Q9MZQ8	Q9mzq8 lepus calif
41	7	3.2	120	2	Q8R1S5	Q8r1s5 mus musculu
42	7	3.2	124	2	Q83XD6	Q83xd6 xanthomonas
43	7	3.2	130	2	Q9Y8R6	Q9y8r6 aeropyrum p
44	7	3.2	131	2	Q8C339	Q8c339 mus musculu
45	7	3.2	132	2	Q9C9P6	Q9c9p6 arabidopsis
46	7	3.2	133	2	O59454	O59454 pyrococcus
47	7	3.2	134	1	Y605 METJA	Y605 METJA
48	7	3.2	134	2	Q6ZSD3	Q6zsd3 methanococc
49	7	3.2	135	2	Q70MM1	Q70mm1 crasseotrea
50	7	3.2	145	2	Q9MZQ5	Q9mzq5 oryctolagus
51	7	3.2	145	2	Q8C383	Q8c383 mus musculu
52	7	3.2	173	2	Q6M9B0	Q6m9b0 neuropora
53	7	3.2	177	2	Q7PMC0	Q7pmc0 anopheles g
54	7	3.2	181	2	Q9NF98	Q9nf98 plasmodium
55	7	3.2	182	2	Q9P5V8	Q9p5v8 neuropora
56	7	3.2	185	2	Q7RVZ3	Q7rvz3 neuropora
57	7	3.2	197	2	Q6ZTI9	Q6zti9 homo sapien
58	7	3.2	206	2	Q89MZ6	Q89mz6 bradyrhizob
59	7	3.2	208	1	RR9 ARATH	RR9 ARATH
60	7	3.2	208	2	Q67Y29	Q67y29 arabidopsis
61	7	3.2	208	2	Q681V1	Q681v1 arabidopsis
62	7	3.2	217	2	Q8C4F8	Q8c4f8 mus musculu
63	7	3.2	223	2	Q72YM4	Q72ym4 bacillus ce
64	7	3.2	223	2	Q6AQZ9	Q6aqz9 desulfotale
65	7	3.2	240	2	Q9KFO9	Q9kfg9 bacillus ha
66	7	3.2	241	2	Q9MZB1	Q9mzr1 oryctolagus
67	7	3.2	257	2	Q64S01	Q64sj1 bacteroides
68	7	3.2	263	2	Q821H3	Q821h3 chlamydomoni
69	7	3.2	265	2	Q9YTM3	Q9ytm3 ateline her
70	7	3.2	271	1	RRF SPIOL	RRF231 spinacia ol
71	7	3.2	275	2	O6FX56	O6fx56 candida gla
72	7	3.2	275	2	Q8S5P7	Q8s5p7 oryza sativ
73	7	3.2	276	2	Q7XB79	Q7xb79 oryza sativ
74	7	3.2	277	1	O24686	O24686 bacillus su
75	7	3.2	279	1	LGT STAAH	LGT STAAH
76	7	3.2	279	1	LGT STAAH	P60962 staphylococ
77	7	3.2	279	1	LGT STAAU	P60963 staphylococ
78	7	3.2	279	1	LGT STAAW	Q8nxl8 staphylococ
79	7	3.2	279	2	Q6GB69	Q6gb69 staphylococ
80	7	3.2	280	2	Q6GIN0	Q6gin0 staphylococ
81	7	3.2	283	1	AROE XANAC	AROE XANAC
82	7	3.2	283	2	Q9L539	Q9l539 xanthomonas
83	7	3.2	284	2	O6TV51	O6tv51 bacillus me
84	7	3.2	290	1	OXAA STAAH	Oxaa STAAH
85	7	3.2	290	1	OXAA STAAH	P85628 staphylococ
86	7	3.2	290	1	OXAA STAAW	P85629 staphylococ
87	7	3.2	290	2	Q6G7M0	Q6g7m0 staphylococ
88	7	3.2	290	2	O6GEY5	O6gey5 staphylococ
89	7	3.2	291	2	Q8LQ63	Q8lq63 oryza sativ
90	7	3.2	293	2	Q8XWT4	Q8xwt4 raistonia s
91	7	3.2	295	2	Q7VSV0	Q7vsv0 bordetella
92	7	3.2	295	2	Q7W3R3	Q7wf41 bordetella
93	7	3.2	295	2	Q89GH7	Q89gh7 bradyrhizob
94	7	3.2	297	2	O17553	O17553 caenorhabdi
95	7	3.2	301	2	O06849	O06849 rhodobacter
96	7	3.2	303	2	O34780	O34780 bacillus su
97	7	3.2	307	2	O5AT HUMAN	O5at HUMAN
98	7	3.2	309	1	Q755P3	Q755p3 ashbya goss
99	7	3.2	317	2	Q755E3	Q755e3 plasmodium
100	7	3.2	321	2	Q7RNE6	Q7rne6 plasmodium
101	7	3.2	322	2	Q7VAR7	Q7var7 prochloroco
102	7	3.2	326	1	NU37 HUMAN	NU37 HUMAN
103	7	3.2	326	1	NU37 MOUSE	NU37 mouse mus musculu
104	7	3.2	326	2	Q9L8N6	Q9l8n6 haemophilus

105	7	3.2	326	2	Q9CZ80	Q9cz80 m. mus muscu	178	7	3.2	485	2	Q8M9F1	O8m9f1 luzula mult
106	7	3.2	329	2	Q7UEV0	Q7uev0 rhodopirell	179	7	3.2	492	2	Q7RZ74	Q7rz74 neurospora
107	7	3.2	332	2	Q72Q99	Q72qp9 leptospira	180	7	3.2	502	2	Q64IW9	Q64iw9 fundulus he
108	7	3.2	332	2	Q8F5E2	Q8f5e2 leptospira	181	7	3.2	505	2	Q98QG8	Q98qg8 rhizobium l
109	7	3.2	335	2	Q648E6	Q648e6 uncultured	182	7	3.2	508	2	Q64IX0	Q64ix0 fundulus he
110	7	3.2	335	2	Q72P82	Q72ps2 leptospira	183	7	3.2	516	2	Q6K975	Q6k975 oryza sativ
111	7	3.2	335	2	Q8CVF2	Q8cvf2 leptospira	184	7	3.2	520	2	Q6H4F1	Q6h4f1 oryza sativ
112	7	3.2	338	2	Q6IF96	Q6if96 homo sapien	185	7	3.2	521	2	Q74DZ3	Q74dz3 geobacter s
113	7	3.2	353	2	Q68DY6	Q68dy6 homo sapien	186	7	3.2	526	2	Q6MIC6	Q6mic6 dellovibri
114	7	3.2	366	2	Q23103	Q23103 caenorhabdi	187	7	3.2	532	2	Q65DE0	Q65de0 bacillus li
115	7	3.2	366	2	Q7V671	Q7v671 prochloroco	188	7	3.2	540	2	Q8GX33	Q8gx33 arabidopsis
116	7	3.2	369	2	Q6TAB5	Q6tab5 symbiont ba	189	7	3.2	541	2	P89039	P89039 la piedad-m
117	7	3.2	372	2	Q6ZPH0	Q6zph0 mus musculu	190	7	3.2	547	2	Q64IX2	Q64ix2 fundulus he
118	7	3.2	373	2	Q8VNT7	Q8vnt7 enterobacte	191	7	3.2	560	2	Q7WX30	Q7wx30 alcaigenes
119	7	3.2	376	2	Q8HDC3	Q8hdc3 pediatrum	192	7	3.2	573	2	Q9XIK1	Q9xik1 arabidopsis
120	7	3.2	377	1	CYCI_HUMAN	Q14094 homo sapien	193	7	3.2	574	2	Q9GRK6	Q9grk6 leishmania
121	7	3.2	377	1	CYCI_MOUSE	Q922v9 mus musculu	194	7	3.2	578	2	Q98M0	Q98m0 clostridium
122	7	3.2	377	2	Q6FH0	Q6fhh0 homo sapien	195	7	3.2	584	2	Q9V825	Q9v825 drosophila
123	7	3.2	377	2	Q8C7E2	Q8c7e2 mus musculu	196	7	3.2	584	2	Q8RXP2	Q8rxp2 arabidopsis
124	7	3.2	377	2	Q99LF2	Q99lf2 mus musculu	197	7	3.2	585	2	Q8HIF3	Q8hif3 arabidopsis
125	7	3.2	381	2	Q8RML4	Q8rml4 enterobacte	198	7	3.2	587	1	CO8B_ONCMY	Q90x85 oncorhynch
126	7	3.2	382	2	Q9KLP1	Q9klp1 vibrio chol	199	7	3.2	588	2	Q8IHE8	Q8ihe8 drosophila
127	7	3.2	385	2	Q89F02	Q89f02 bradyrhizob	200	7	3.2	596	2	Q7SXS7	Q7sxs7 brachydanio
128	7	3.2	386	2	Q6XQM9	Q6xqm9 gallus gall	201	7	3.2	597	2	Q8NC94	Q8nc94 homo sapien
129	7	3.2	389	2	Q8TN02	Q8tn02 methanosarc	202	7	3.2	599	2	Q9FY0	Q9fy0 pseudomonas
130	7	3.2	391	2	Q82KV8	Q82kv8 streptomyce	203	7	3.2	602	2	Q83B1	Q83b1 enterococcu
131	7	3.2	392	1	YUXJ_BACSU	P40760 bacillus su	204	7	3.2	603	2	Q9SSB2	Q9ssb2 arabidopsis
132	7	3.2	401	2	Q8WQ40	Q8wq40 leishmania	205	7	3.2	608	2	Q8BKA3	Q8bka3 m mus muscu
133	7	3.2	404	2	Q9J897	Q9j897 spodoptera	206	7	3.2	614	2	Q8YC41	Q8yc41 bruceella me
134	7	3.2	407	2	Q876V9	Q876v9 grifola umb	207	7	3.2	615	2	Q8FW84	Q8fw84 bruceella su
135	7	3.2	408	2	Q6FSI7	Q6fsi7 candida gla	208	7	3.2	625	2	Q6BI61	Q6bi61 debaryomyce
136	7	3.2	409	2	Q73GCS	Q73gcs wolbachia p	209	7	3.2	632	2	Q64ZHI	Q64zh1 brachydanio
137	7	3.2	410	2	Q8TU92	Q8tu92 methanosarc	210	7	3.2	642	2	Q9DHT6	Q9dht6 yaba-like d
138	7	3.2	412	2	Q68EL9	Q68el9 brachydanio	211	7	3.2	659	2	Q8UJH3	Q8ujh3 pyrococcus
139	7	3.2	416	2	Q65JZ6	Q65jz6 bacillus li	212	7	3.2	663	1	GLI3_CHICK	P55879 gallus gall
140	7	3.2	417	2	Q6NTW1	Q6ntw1 xenopus lae	213	7	3.2	664	2	Q8RV6	Q8rbv6 thermoanaer
141	7	3.2	419	2	Q80UP6	Q80uf6 mus musculu	214	7	3.2	670	2	Q89EX0	Q89ex0 clostridium
142	7	3.2	420	2	Q9PUM7	Q9pum7 xenopus lae	215	7	3.2	683	2	Q6BYR0	Q6byr0 debaryomyce
143	7	3.2	421	2	Q80G96	Q80g96 arabidopsis	216	7	3.2	689	2	Q95Y73	Q95y73 caenorhabdi
144	7	3.2	425	2	Q7UXZ5	Q7uxz5 rhodopirell	217	7	3.2	701	2	P91922	P91922 calliphora
145	7	3.2	425	2	Q8VDP1	Q8vdp1 mus musculu	218	7	3.2	727	2	Q86KB4	Q86kb4 dictyosteli
146	7	3.2	427	2	Q80Y55	Q80y55 mus musculu	219	7	3.2	732	2	Q7RXT7	Q7rxt7 neurospora
147	7	3.2	427	2	Q8BI04	Q8bi04 mus musculu	220	7	3.2	757	2	Q90WS0	Q90ws0 fugu rubrip
148	7	3.2	430	2	Q6IAA3	Q6iaa3 homo sapien	221	7	3.2	770	2	Q8YMK4	Q8ymk4 anabaena sp
149	7	3.2	430	2	Q9NWE8	Q9nw68 homo sapien	222	7	3.2	777	2	Q6CFP0	Q6cfp0 kluyveromyc
150	7	3.2	431	2	Q72WD7	Q72wd7 desulfovibr	223	7	3.2	779	2	Q9UI21	Q9ui21 leishmania
151	7	3.2	433	2	Q8GU14	Q8gu14 arabidopsis	224	7	3.2	791	2	Q8CUG5	Q8cug5 oceanobacil
152	7	3.2	437	2	Q6AML4	Q6aml4 desulfotale	225	7	3.2	812	2	Q9PSZ4	Q9ps24 gallus gall
153	7	3.2	438	2	Q7PYK2	Q7pyk2 anopheles g	226	7	3.2	827	2	Q6H8R9	Q6h8r9 ustilago ma
154	7	3.2	440	2	Q94A02	Q94a02 arabidopsis	227	7	3.2	828	2	Q6Z469	Q6z469 oryza sativ
155	7	3.2	441	1	YK17_SCHPO	Q94y3 schizosacch	228	7	3.2	863	1	GLND_HABIN	P43919 haemophilus
156	7	3.2	444	2	Q6CG06	Q6cg06 yarrowia li	229	7	3.2	864	1	GLND_PASMU	Q9cnh1 pasteurella
157	7	3.2	444	2	Q8YZS1	Q8yzs1 anabaena sp	230	7	3.2	868	2	Q6D3J0	Q6d3j0 erwinia car
158	7	3.2	449	2	Q8IHW3	Q8ihw3 plasmodium	231	7	3.2	885	2	Q6FKB4	Q6fkb4 candida gla
159	7	3.2	452	2	Q7R2X5	Q7r2x5 giardia lam	232	7	3.2	889	2	Q8XMY3	Q8xmy3 clostridium
160	7	3.2	454	2	Q64IX1	Q64ix1 fundulus he	233	7	3.2	904	1	MLK2_HUMAN	Q8iy33 homo sapien
161	7	3.2	455	2	Q6GLY2	Q6gl712 bifidobacte	234	7	3.2	920	1	AD19_MOUSE	Q35674 mus musculu
162	7	3.2	457	2	Q6LHY2	Q6lhy2 photobacter	235	7	3.2	932	2	P89499	P89499 saccharomyc
163	7	3.2	460	2	Q9H8M0	Q9h8m0 homo sapien	236	7	3.2	939	2	Q64XK8	Q64xk8 bacteroides
164	7	3.2	461	2	Q8GQ90	Q8gq90 pseudomonas	237	7	3.2	943	2	Q8E566	Q8ee56 shewanella
165	7	3.2	465	2	Q93Q44	Q93q44 clostridium	238	7	3.2	946	1	YBT5_YEAST	P38250 saccharomyc
166	7	3.2	466	1	ATPB_CLOAB	Q92687 clostridium	239	7	3.2	947	1	MUSK_CHICK	Q8ax66 gallus gall
167	7	3.2	467	2	Q8XHZ3	Q8xhz3 clostridium	240	7	3.2	962	2	Q75CM3	Q75cm3 ashpya goss
168	7	3.2	467	2	Q6NF08	Q6nfq8 corynebacte	241	7	3.2	962	2	Q8PUK6	Q8puk6 methanosarc
169	7	3.2	470	2	Q7NF68	Q7nf68 gloebobacter	242	7	3.2	963	2	Q80VY5	Q80vy5 mus musculu
170	7	3.2	471	2	Q8GVN3	Q8gvn3 oryza sativ	243	7	3.2	964	2	Q9VNM2	Q9vnm2 lymantria d
171	7	3.2	473	2	Q65N12	Q65n12 bacillus li	244	7	3.2	985	2	Q6ES98	Q6es98 oryza sativ
172	7	3.2	474	2	Q6MZK1	Q6mzk1 homo sapien	245	7	3.2	998	1	S231_MOUSE	Q6nzc7 mus musculu
173	7	3.2	475	2	Q8GVN0	Q8gvn0 oryza sativ	246	7	3.2	1000	1	S231_HUMAN	Q9gy68 homo sapien
174	7	3.2	476	2	Q978K1	Q978k1 thermoplasm	247	7	3.2	1014	2	Q9SHF3	Q9shf3 arabidopsis
175	7	3.2	479	2	Q7NVG3	Q7nvq3 chromobacte	248	7	3.2	1084	2	Q86IA6	Q86ia6 dictyosteli
176	7	3.2	480	2	Q90220	Q90220 agkistrodon	249	7	3.2	1123	2	Q6ZL37	Q6z137 oryza sativ
177	7	3.2	482	2	Q6BS29	Q6bs29 debaryomyce	250	7	3.2	1144	2	Q6M9R8	Q6m9r8 parachlamyid

251	7	3.2	1145	2	QC7Y9	Q6c7y9	yarrowia li
252	7	3.2	1247	2	QCCLKO	Q6clko	kluyveromyc
253	7	3.2	1257	1	PCCN RAT	P5067	rattus norv
254	7	3.2	1258	1	GLI2 HUMAN	P10070	homo sapien
255	7	3.2	1266	2	ORGU80	Q8gu80	oryza sativ
256	7	3.2	1268	1	PCCN MOUSE	P5066	mus musculus
257	7	3.2	1268	2	Q6P1E3	Q6pie3	mus musculus
258	7	3.2	1274	2	Q9S2B7	Q9ez87	arabidopsis
259	7	3.2	1281	2	Q8TSN6	Q8tsn6	methanosarc
260	7	3.2	1284	2	Q23974	Q23974	drosophila
261	7	3.2	1284	2	Q3V899	Q3v899	drosophila
262	7	3.2	1286	2	QYR74	QYr74	macaca mula
263	7	3.2	1321	1	PCCN HUMAN	Q4594	homo sapien
264	7	3.2	1326	2	Q9VZF4	Q9vzf4	drosophila
265	7	3.2	1354	2	Q9W6B2	Q9w6b2	xenopus lae
266	7	3.2	1356	2	Q9NEB8	Q9neb8	leishmania
267	7	3.2	1359	2	Q752W3	Q752w3	ashbya goss
268	7	3.2	1361	2	Q9NGV2	Q9ngv2	drosophila
269	7	3.2	1361	2	Q9V714	Q9v714	drosophila
270	7	3.2	1609	1	FIG2 YEAST	P25653	saccharomyc
271	7	3.2	1683	1	LM07 HUMAN	Q8ww11	homo sapien
272	7	3.2	1721	2	Q835J4	Q835a4	enterococcu
273	7	3.2	1734	2	Q8MKW9	Q8mkw9	drosophila
274	7	3.2	1743	2	Q966V0	Q966v0	drosophila
275	7	3.2	1842	2	Q6CUT9	Q6cut9	kluyveromyc
276	7	3.2	2205	2	Q7KRf5	Q7krf5	drosophila
277	7	3.2	2237	2	Q7RQ19	Q7rqi9	plasmodium
278	7	3.2	2515	2	Q24551	Q24551	drosophila
279	7	3.2	2555	2	Q8T9E3	Q8t9e3	drosophila
280	7	3.2	2559	2	Q44113	Q44113	drosophila
281	7	3.2	2559	2	Q44381	Q44381	drosophila
282	7	3.2	2559	2	Q9V7X3	Q9v7x3	drosophila
283	7	3.2	2633	2	Q7OK12	Q7gk12	anopheles g
284	7	3.2	2669	2	Q9MY8	Q9my8	mus musculus
285	7	3.2	2671	2	Q754J3	Q754a3	ashbya goss
286	7	3.2	2731	2	Q18366	Q18366	drosophila
287	7	3.2	2731	2	Q61307	Q61307	drosophila
288	7	3.2	2731	2	Q9VNU6	Q9vnu6	drosophila
289	7	3.2	2870	2	Q97Lr2	Q97lf2	clostridium
290	7	3.2	2969	2	Q5NR48	Q5nr48	homo sapien
291	7	3.2	2974	2	Q815L7	Q815l7	plasmodium
292	7	3.2	3153	2	Q6C6F9	Q6c6f9	yarrowia li
293	7	3.2	3469	2	Q9U412	Q9u412	drosophila
294	7	3.2	3604	2	Q9VYK0	Q9vyk0	drosophila
295	7	3.2	3657	2	Q96QJ5	Q96q15	homo sapien
296	7	3.2	3684	1	UPL1 ARATH	Q8gy23	arabidopsis
297	7	3.2	4753	2	Q8PLI3	Q8pli3	xanthomonas
298	7	3.2	6315	2	Q9ADL6	Q9adl6	polyangium
299	7	3.2	6973	2	Q7QXR7	Q7qxr7	giardia lam
300	6	2.8	25	2	Q6QH14	Q6ghi4	leptosphaer
301	6	2.8	27	2	Q91JF4	Q91jf4	hepatitis c
302	6	2.8	32	2	Q44509	Q44509	azotobacter
303	6	2.8	33	2	Q7M1R4	Q7mlr4	spinacia ol
304	6	2.8	38	2	Q7P8V1	Q7p8v1	rickettsia
305	6	2.8	41	2	Q739F1	Q739f1	bacillus ce
306	6	2.8	46	2	Q87NG9	Q87ng9	vibrio para
307	6	2.8	47	2	Q23578	Q23578	caenorhabdi
308	6	2.8	48	2	Q9AIN3	Q9ain3	streptococc
309	6	2.8	48	2	Q879N9	Q879n9	streptococc
310	6	2.8	48	2	Q9Q577	Q9q577	human immun
311	6	2.8	49	2	Q811J1	Q811j1	drosophila
312	6	2.8	49	2	Q9Q578	Q9q578	human immun
313	6	2.8	49	2	Q9Q580	Q9q580	human immun
314	6	2.8	50	2	Q9PG59	Q9pg59	xytella fas
315	6	2.8	50	2	Q65342	Q65342	autographa
316	6	2.8	55	2	Q96X16	Q96xl6	sulfolobus
317	6	2.8	55	2	Q67KQ3	Q67kq3	symbiobacte
318	6	2.8	55	2	Q83EJ5	Q83ej5	coxiella bu
319	6	2.8	56	2	Q8K9E1	Q8k9e1	bacillus ha
320	6	2.8	58	2	Q44EL5	Q44el5	uncultured
321	6	2.8	59	2	Q41936	Q41936	arabidopsis
322	6	2.8	59	2	Q81R19	Q81r19	bacillus an
323	6	2.8	61	2	Q6K483	Q6k483	oryza sativ

324	6	2.8	61	2	Q99MQ6	Q99mq6	cricketulus
325	6	2.8	63	1	SIFA MAIZE	P42554	zea mays (m
326	6	2.8	64	2	Q91Y98	Q91y98	mus musculu
327	6	2.8	65	2	Q6LTF6	Q6ltf6	photobacter
328	6	2.8	65	2	Q91QZ5	Q91qz5	cercopithec
329	6	2.8	68	2	Q7QCP5	Q7qct5	giardia lam
330	6	2.8	69	1	COFZ ENTHR	Q47840	enterococcu
331	6	2.8	70	2	Q7Z4B4	Q7z4b4	homo sapien
332	6	2.8	70	2	Q6H2R5	Q6hzr5	bacillus an
333	6	2.8	70	2	Q63CB1	Q63cb1	bacillus ce
334	6	2.8	70	2	Q7W9G7	Q7w9g7	bordetella
335	6	2.8	70	2	Q7WH95	Q7wh95	bordetella
336	6	2.8	70	2	Q9CKF1	Q9ckp1	pasteurella
337	6	2.8	70	2	Q6HJS3	Q6hjs3	bacillus th
338	6	2.8	71	2	Q63UR7	Q63ur7	burkholderi
339	6	2.8	71	2	Q7NSV8	Q7nsv8	chromobacte
340	6	2.8	71	2	Q9PI59	Q9pi59	campylobact
341	6	2.8	72	2	Q7PRD3	Q7prd3	anopheles g
342	6	2.8	72	2	Q81EE1	Q81eel	bacillus ce
343	6	2.8	72	2	Q86918	Q86918	human t-lym
344	6	2.8	73	2	Q7PQH8	Q7pqh8	anopheles g
345	6	2.8	73	2	Q7PUZ9	Q7puz9	anopheles g
346	6	2.8	73	2	Q6Z586	Q6z586	peromyseus
347	6	2.8	73	2	Q64372	Q64372	peromyseus
348	6	2.8	74	2	Q9LLN8	Q9lln8	oryza sativ
349	6	2.8	74	2	Q7MSL5	Q7msl5	wolinnella s
350	6	2.8	74	2	Q7WBF5	Q7wbf5	bordetella
351	6	2.8	74	2	Q7WMX6	Q7wmx6	bordetella
352	6	2.8	75	2	Q6AX78	Q6ax78	xenopus lae
353	6	2.8	79	2	Q7PE02	Q7pe02	anopheles g
354	6	2.8	79	2	Q7PEF7	Q7pef7	anopheles g
355	6	2.8	79	2	Q7PIW0	Q7piw0	anopheles g
356	6	2.8	82	2	Q7YX33	Q7yx33	caenorhabdi
357	6	2.8	82	2	Q22634	Q22634	oryza sativ
358	6	2.8	82	2	Q6K3Y6	Q6k3y6	oryza sativ
359	6	2.8	85	2	Q64660	Q64660	cavia (guin
360	6	2.8	85	2	Q80844	Q80844	hantavirus
361	6	2.8	88	2	Q8RZG8	Q8rzg8	oryza sativ
362	6	2.8	89	1	PERC ECO27	P43475	escherichia
363	6	2.8	89	2	Q8S6T9	Q8s6t9	oryza sativ
364	6	2.8	89	2	Q7Y1K5	Q7y1k5	oryza sativ
365	6	2.8	89	2	Q9APE4	Q9ape4	escherichia
366	6	2.8	89	2	Q9EUG3	Q9eug3	escherichia
367	6	2.8	89	2	Q9F874	Q9f874	escherichia
368	6	2.8	89	2	Q9F883	Q9f883	escherichia
369	6	2.8	89	2	Q7DJ53	Q7dj53	escherichia
370	6	2.8	90	2	Q8W2H5	Q8w2h5	setaria ver
371	6	2.8	90	2	Q8W2J0	Q8w2j0	setaria fab
372	6	2.8	91	1	UTER HUMAN	P11684	homo sapien
373	6	2.8	91	2	Q6FJ46	Q6fj46	candida gla
374	6	2.8	91	2	Q9BNQ8	Q9bnq8	milnesium t
375	6	2.8	91	2	Q75LQ5	Q75lq5	oryza sativ
376	6	2.8	91	2	Q72749	Q72749	human immun
377	6	2.8	92	2	Q6ARR7	Q6arr7	desulfotale
378	6	2.8	93	2	Q6ESP6	Q6esp6	oryza sativ
379	6	2.8	93	2	Q7BV71	Q7bv71	salmonella
380	6	2.8	93	2	Q6LJ48	Q6lj48	photobacter
381	6	2.8	93	2	Q75382	Q75382	human immun
382	6	2.8	95	2	Q7KUG7	Q7kug7	drosophila
383	6	2.8	96	2	Q92EAI	Q92eal	listeria in
384	6	2.8	96	2	Q83JN4	Q83jn4	shigella fl
385	6	2.8	97	2	Q7RDA7	Q7rda7	plasmodium
386	6	2.8	97	2	Q62JY2	Q62jy2	burkholderi
387	6	2.8	98	2	Q22789	Q22789	arabidopsis
388	6	2.8	98	2	Q82R21	Q82r21	streptomyce
389	6	2.8	99	2	Q7DDB1	Q7ddb1	neisseria m
390	6	2.8	99	2	Q9JR93	Q9jlr93	neisseria m
391	6	2.8	100	2	Q58249	Q58249	pyrococcus
392	6	2.8	100	2	Q8GVH1	Q8gvh1	oryza sativ
393	6	2.8	100	2	Q6GM33	Q6gm33	xenopus lae
394	6	2.8	101	2	Q14476	Q14476	homo sapien
395	6	2.8	101	2	Q9VDS4	Q9vds4	drosophila
396	6	2.8	101	2	Q86332	Q86332	mycobacteri

397	6	2.8	101	2	Q7U194	Q7u194 mycobacteri	470	6	2.8	116	2	Q6XFX2	O6xfx2 nectarinia
398	6	2.8	101	2	Q9C723	Q9ctz3 mus musculu	471	6	2.8	116	2	Q6XFX5	O6xfx5 nectarinia
399	6	2.8	101	2	Q8QVL7	Q8qv17 tt virus. o	472	6	2.8	116	2	Q6XFX9	O6xfx9 nectarinia
400	6	2.8	102	1	YAC1 MAIZE	P08771 zea mays (m	473	6	2.8	116	2	Q6XFY0	O6xfy0 nectarinia
401	6	2.8	102	2	Q8KG24	Q8kg24 chlorobium	474	6	2.8	116	2	Q6XFY1	O6xfy1 anthrepes
402	6	2.8	102	2	Q64098	Q64098 mus sp. tru	475	6	2.8	116	2	Q8GI75	O8gi75 salmonella
403	6	2.8	103	2	Q9YAP0	Q9yap0 aeropyrum p	476	6	2.8	116	2	Q8V2N5	O8v2n5 camelpox vi
404	6	2.8	103	2	Q6GMW9	Q6gmw9 homo sapien	477	6	2.8	116	2	Q6ZV15	O6zv15 pyrobaculum
405	6	2.8	104	1	F5PE ECOLI	P23857 escherichia	478	6	2.8	116	2	Q775Q6	O775q6 camelpox vi
406	6	2.8	104	2	Q42216	Q42216 arabidopsis	479	6	2.8	116	2	Q9JF81	Q9jfb1 vaccinia vi
407	6	2.8	104	2	Q8CW40	Q8cw40 escherichia	480	6	2.8	117	1	VA21_VACCC	P20996 vaccinia vi
408	6	2.8	104	2	Q8D8D5	Q8d8d5 vibrio vuln	481	6	2.8	117	1	VA21_VARV	P33844 variola vir
409	6	2.8	105	2	Q828D3	Q828d3 pseudomonas	482	6	2.8	117	2	Q975F3	Q975f3 sulfolobus
410	6	2.8	105	2	Q8GI15	Q8gi15 pseudomonas	483	6	2.8	117	2	Q871K4	Q871k4 neurospora
411	6	2.8	105	2	Q739J5	Q739j5 bacillus ce	484	6	2.8	117	2	Q9GKU0	Q9gku0 macaca fasc
412	6	2.8	105	2	Q924A3	Q924a3 mus musculu	485	6	2.8	117	2	Q9CBX5	Q9cbx5 mycobacteri
413	6	2.8	105	2	Q8C5P4	Q8c5p4 mus musculu	486	6	2.8	117	2	Q8QMT3	Q8qmt3 cowpox viru
414	6	2.8	106	2	Q70M31	Q70m31 natronomona	487	6	2.8	117	2	Q6RZG2	Q6rzg2 rabbitpox v
415	6	2.8	106	2	Q70M33	Q70m33 halorubrum	488	6	2.8	117	2	Q76PY0	Q76py0 variola min
416	6	2.8	106	2	Q84N88	Q84n88 cadia purpu	489	6	2.8	117	2	Q76QI6	Q76qi6 cowpox viru
417	6	2.8	107	2	Q8WY21	Q8wy21 homo sapien	490	6	2.8	117	2	Q762P8	Q76p8 vaccinia vi
418	6	2.8	108	2	Q7RT15	Q7rt15 plasmodium	491	6	2.8	118	2	Q97Z66	Q97z66 sulfolobus
419	6	2.8	109	2	Q7PHS4	Q7phs4 anopheles g	492	6	2.8	118	2	Q21028	Q21028 caenorhabdi
420	6	2.8	109	2	Q7Q7U1	Q7q7u1 anopheles g	493	6	2.8	118	2	Q6YPX1	Q6ypx1 onion yello
421	6	2.8	109	2	Q9BPJ0	Q9bpj0 campylobact	494	6	2.8	118	2	Q8JL94	O8jl94 ectromelia
422	6	2.8	110	2	Q85SP1	Q85sp1 mycobacteri	495	6	2.8	119	2	Q61LI0	O61li0 drosophila
423	6	2.8	110	2	Q8DLH7	Q8dlh7 synecococc	496	6	2.8	120	2	Q8PVB8	O8pvb8 methanosarc
424	6	2.8	111	2	Q6ZNNK0	Q6znnk0 homo sapien	497	6	2.8	120	2	Q6YTR4	O6ytr4 oryza sativ
425	6	2.8	111	2	Q6DY61	Q6dy61 nectarinia	498	6	2.8	120	2	Q82XB7	O82xb7 nitrosomona
426	6	2.8	111	2	Q6DY62	Q6dy62 nectarinia	499	6	2.8	121	2	Q93XR8	Q93xr8 bruguiera g
427	6	2.8	111	2	Q6DY64	Q6dy64 nectarinia	500	6	2.8	121	2	Q67UU3	O67u3 oryza sativ
428	6	2.8	111	2	Q6DY65	Q6dy65 nectarinia	501	6	2.8	121	2	Q84N74	O84n74 machaerium
429	6	2.8	111	2	Q6DY66	Q6dy66 nectarinia	502	6	2.8	121	2	Q7V1P5	Q7v1p5 prochloroco
430	6	2.8	111	2	Q6DY98	Q6dy98 nectarinia	503	6	2.8	121	2	Q8FLM2	Q8flm2 corynebacte
431	6	2.8	111	2	Q6DYA1	Q6dya1 nectarinia	504	6	2.8	121	2	Q6MCZ2	O6mcz2 parachlamyd
432	6	2.8	111	2	Q6DYA2	Q6dya2 nectarinia	505	6	2.8	121	2	Q66897	O66897 four corner
433	6	2.8	111	2	Q6DYA5	Q6dya5 nectarinia	506	6	2.8	122	2	Q62H83	O62h83 oryza sativ
434	6	2.8	111	2	Q76Z05	Q76z05 bacterioph	507	6	2.8	122	2	Q6LSG5	O6ls5 photobacter
435	6	2.8	112	2	Q8GU28	Q8gu28 polytomella	508	6	2.8	123	2	Q14474	O14474 homo sapien
436	6	2.8	113	2	Q64C64	Q64c64 uncultured	509	6	2.8	123	2	Q8FG00	O8fg00 escherichia
437	6	2.8	113	2	Q57817	O57817 pyrococcus	510	6	2.8	123	2	Q8X7I0	O8x7i0 escherichia
438	6	2.8	113	2	Q8TNN3	O8tnn3 methanosarc	511	6	2.8	123	2	Q83KI3	O83ki3 shigella fl
439	6	2.8	113	2	Q8ZZP8	Q8zzp8 pyrobaculum	512	6	2.8	124	2	Q7Y597	O7y597 bacterioph
440	6	2.8	113	2	Q86XP5	Q86xp5 homo sapien	513	6	2.8	126	2	Q8TS70	O8ts70 methanosarc
441	6	2.8	113	2	Q7PEP9	Q7pep9 anopheles g	514	6	2.8	126	2	Q6ZT32	O6zt32 homo sapien
442	6	2.8	113	2	Q6AA9Y	Q6aay9 propionibac	515	6	2.8	126	2	Q8CT85	O8ct85 staphylococ
443	6	2.8	113	2	Q8DAJ3	Q8daj3 vibrio vuln	516	6	2.8	126	2	Q8C517	O8c517 mus musculu
444	6	2.8	114	1	YHT8 YEAST	P38841 saccharomyc	517	6	2.8	126	2	Q73616	O73616 xenopus lae
445	6	2.8	114	2	Q6XFG9	Q6xf9 nectarinia	518	6	2.8	127	2	Q856G8	O856g8 mycobacteri
446	6	2.8	114	2	Q6ETH8	Q6eth8 oryza sativ	519	6	2.8	128	2	Q8N7N0	O8n7n0 homo sapien
447	6	2.8	114	2	Q81PU2	Q8ip12 bacillus an	520	6	2.8	128	2	Q9EVJ5	O9evj5 edta-degrad
448	6	2.8	115	2	Q6XFP0	Q6xf0 nectarinia	521	6	2.8	129	2	Q9UNL6	Q9unl6 homo sapien
449	6	2.8	115	2	Q6XFH2	Q6xfh2 nectarinia	522	6	2.8	129	2	Q7QX87	O7qx87 giardia lam
450	6	2.8	115	2	Q6HHT1	Q6hht1 bacillus th	523	6	2.8	129	2	Q9IZL0	O9izl0 simian t-ly
451	6	2.8	115	2	Q83RL0	Q83rl0 shigella fl	524	6	2.8	130	2	Q9YCB5	O9ycb5 aeropyrum p
452	6	2.8	115	2	Q8V4V7	Q8v4v7 monkeypox v	525	6	2.8	131	2	Q70AI5	O70a5 triticum ae
453	6	2.8	116	2	Q6JGM0	Q6jgm0 todistrogm	526	6	2.8	131	2	Q83E98	O83e98 coxiella bu
454	6	2.8	116	2	Q6XFP4	Q6xf4 nectarinia	527	6	2.8	132	1	RR12_CHLRE	P14149 chlamydomon
455	6	2.8	116	2	Q6XFP5	Q6xf5 nectarinia	528	6	2.8	132	2	Q70JC2	O70jc2 bacillus li
456	6	2.8	116	2	Q6XFP6	Q6xf6 nectarinia	529	6	2.8	132	2	Q98B24	O98b24 rhizobium l
457	6	2.8	116	2	Q6XFP7	Q6xf7 nectarinia	530	6	2.8	132	2	Q8U0R1	O8u0r1 pyrococcus
458	6	2.8	116	2	Q6XFP4	Q6xf4 nectarinia	531	6	2.8	133	2	Q21887	O21887 caenorhabdi
459	6	2.8	116	2	Q6XFP5	Q6xf5 nectarinia	532	6	2.8	133	2	Q6H4G7	O6h4g7 oryza sativ
460	6	2.8	116	2	Q6XFP6	Q6xf6 nectarinia	533	6	2.8	133	2	Q92GJ7	O92gj7 rickettsia
461	6	2.8	116	2	Q6XFP8	Q6xf8 nectarinia	534	6	2.8	133	2	Q9CRX9	O9crx9 mus musculu
462	6	2.8	116	2	Q6XFG1	Q6xf1 nectarinia	535	6	2.8	134	2	Q8T352	O8t352 plasmodium
463	6	2.8	116	2	Q6XFG4	Q6xf4 nectarinia	536	6	2.8	134	2	Q25078	O25078 helicobacte
464	6	2.8	116	2	Q6XFG7	Q6xf7 nectarinia	537	6	2.8	134	2	Q9ZMC8	O9zmc8 mus musculu
465	6	2.8	116	2	Q6XFG8	Q6xf8 nectarinia	538	6	2.8	134	2	Q9CRZ2	O9crz2 mus musculu
466	6	2.8	116	2	Q6XPH0	Q6xfh0 nectarinia	539	6	2.8	136	2	O62434	O62434 caenorhabdi
467	6	2.8	116	2	Q6XPH3	Q6xfh3 nectarinia	540	6	2.8	136	2	Q7R6A8	O7r6a8 giardia lam
468	6	2.8	116	2	Q6XPH5	Q6xfh5 nectarinia	541	6	2.8	136	2	Q9WNX1	O9wnx1 human t-lym
469	6	2.8	116	2	Q6XFX0	O6xfx0 nectarinia	542	6	2.8	137	2	Q70M34	O70m34 halobacteri

543	138	2	Q6BN70	Q6bn70 debaryomyce	616	6	2.8	146	1	HBG_MACNE	P02097 macaca neme
544	139	2	Q6ZUI3	Q6zui3 homo sapien	617	6	2.8	146	1	HBG_TAPCY	P68079 papio cynoc
545	139	2	Q6GRS1	Q6gra1 hammodium	618	6	2.8	146	1	HBG_TAPCY	P07655 tarsius ban
546	139	2	Q7NFX2	Q7nfx2 gloeobacter	619	6	2.8	146	1	P7FA_BACSU	P26379 bacillus ba
547	140	2	Q59311	Q59311 pyrococcus	620	6	2.8	146	1	Q8GT54	P8454 hordeum vul
548	140	2	Q6ZR24	Q6zr24 homo sapien	621	6	2.8	146	2	Q6TIM6	Q8tlm6 staphylococ
549	140	2	Q6ZVP1	Q6zvp1 homo sapien	622	6	2.8	146	2	Q6TIM7	Q8tlm7 staphylococ
550	140	2	Q8LA12	Q8la12 arabidopsis	623	6	2.8	146	2	Q6TIM1	Q8tlm1 staphylococ
551	140	2	Q93NE0	Q93ne0 myxococcus	624	6	2.8	146	2	Q6TIM3	Q8tlm3 staphylococ
552	140	2	Q87IX2	Q87ix2 vibrio para	625	6	2.8	146	2	Q6TIM4	Q8tlm4 staphylococ
553	141	2	Q6IKR8	Q6ikr8 drosophila	626	6	2.8	146	2	Q6TIM1	Q8tlm1 staphylococ
554	141	2	Q8GX01	Q8gx01 arabidopsis	627	6	2.8	146	2	Q84G94	Q84g94 staphylococ
555	141	2	Q9C7Q8	Q9c7q8 arabidopsis	628	6	2.8	146	2	Q84G95	Q84g95 staphylococ
556	141	2	Q9CMT1	Q9cmt1 mus musculu	629	6	2.8	146	2	Q84G96	Q84g96 staphylococ
557	141	2	Q84663	Q84663 paramacium	630	6	2.8	146	2	Q8F267	Q8f267 leptospira
558	142	1	RL11_BRUME	Q8yhc1 brucella me	631	6	2.8	146	2	Q9QUN8	Q9qun8 mus musculu
559	142	1	RL11_BRUSU	Q8yhc1 brucella su	632	6	2.8	146	2	Q9QUT6	Q9qut6 rattus sp.
560	142	2	Q95233	Q95233 perodicticu	633	6	2.8	146	2	Q9QW91	Q9qw91 rattus sp.
561	142	2	Q6TIN8	Q6tin8 staphylococ	634	6	2.8	146	2	Q9R0S6	Q9r0s6 mus musculu
562	142	2	Q9YMS0	Q9yme0 lymantria d	635	6	2.8	146	2	Q7TIF0	Q7tlf0 geochelone
563	142	2	Q29967	Q29967 lactococcus	636	6	2.8	147	1	HBG_TARSY	Q9f562 escherichia
564	143	2	Q48527	Q48527 arabidopsis	637	6	2.8	147	1	Q96FH6	P18436 tarsius syr
565	143	2	Q82G13	Q82g13 streptomyce	638	6	2.8	147	2	Q96FH7	Q96fh7 homo sapien
566	143	2	Q8D6B9	Q8d6b9 vibrio vuln	639	6	2.8	147	2	Q68NH9	Q68nh9 homo sapien
567	143	2	Q8DAJ2	Q8daj2 vibrio vuln	640	6	2.8	147	2	Q03903	Q03903 macaca mula
568	144	2	Q72K31	Q72k31 thermus the	641	6	2.8	147	2	Q9F562	Q9f562 escherichia
569	145	2	P74671	P74671 synchocyst	642	6	2.8	147	2	Q88752	Q88752 rattus norv
570	145	2	Q6FLX6	Q6flx6 mesoplasma	643	6	2.8	147	2	Q91V86	Q91v86 m mus muscu
571	146	1	HBB1_MOUSE	P02088 mus musculu	644	6	2.8	147	2	Q9CR49	Q9cr49 m mus muscu
572	146	1	HBB1_RAT	P02091 rattus norv	645	6	2.8	147	2	Q9CXH5	Q9cxh5 mus musculu
573	146	1	HBB2_MOUSE	P02089 mus musculu	646	6	2.8	147	2	Q9CY12	Q9cy12 mus musculu
574	146	1	HBB2_RAT	P11517 rattus norv	647	6	2.8	147	2	Q9CY54	Q9cy54 mus musculu
575	146	1	HBB_CAVPO	P02095 cavia porce	648	6	2.8	147	2	Q9D0B2	Q9d0b2 mus musculu
576	146	1	HBB_CYNBP	P11754 cynopterus	649	6	2.8	147	2	Q95W24	Q95w24 anthonomus
577	146	1	HBB_GEONI	P83123 geochelone	650	6	2.8	148	2	Q65142	Q65i42 bacillus li
578	146	1	HBB_MARMA	P08853 marmota mar	651	6	2.8	149	2	Q9GMG9	Q9gm9 macaca mula
579	146	1	HBB_MESAU	P02094 mesocricetu	652	6	2.8	149	2	Q6W3M8	Q6w3m8 alvinella p
580	146	1	HBB_MESBR	P18707 mesocricetu	653	6	2.8	149	2	Q7NIN2	Q7nln2 photorhabdu
581	146	1	HBB_MICXA	P02092 microtus xa	654	6	2.8	149	2	Q9WNX0	Q9wnx0 human t-lym
582	146	1	HBB_PSIKR	P21668 psittacula	655	6	2.8	150	1	TRPE_CITFR	P00896 citrobacter
583	146	1	HBB_PTEAL	P14391 pteropus al	656	6	2.8	150	2	Q6MAN8	Q6man8 parachlamyd
584	146	1	HBB_ROUAE	P02058 roussettu a	657	6	2.8	151	2	Q752P4	Q752p4 haemadipsa
585	146	1	HBB_SPECI	P09421 spermophilu	658	6	2.8	151	2	Q7Y4Z1	Q7y4z1 bacterioph
586	146	1	HBB_SPETO	P07410 spermophilu	659	6	2.8	151	2	Q855Z3	Q855z3 mycobacteri
587	146	1	HBB_SUNMU	P02060 suncus muri	660	6	2.8	151	2	Q8KJQ9	Q8kj99 vibrio angu
588	146	1	HBB_TADBR	P11756 tadarida br	661	6	2.8	151	2	Q8R738	Q8r738 thermocanaer
589	146	1	HBB_TALEU	P02061 talpa europ	662	6	2.8	152	1	V57B_BP74	P04533 bacterioph
590	146	1	HBB_TRIIN	P07415 trichechus	663	6	2.8	152	2	Q14491	Q14491 homo sapien
591	146	1	HBE1_CAPHI	P02102 capra hircu	664	6	2.8	152	2	Q8B571	Q8b571 pseudocowpo
592	146	1	HBE_CHEME	Q28338 cheirogaleu	665	6	2.8	152	2	Q6EEB2	Q6eeb2 latimeria c
593	146	1	HBE_DAUMA	Q28356 daubentonia	666	6	2.8	153	1	Y1BG_ECOLI	P32106 escherichia
594	146	1	HBE_DIDMA	P11025 didelphis m	667	6	2.8	153	2	Q7SGT4	Q7sgt4 neurospora
595	146	1	HBE_EULFU	P08223 eulemur ful	668	6	2.8	153	2	Q8MVN3	Q8mvn3 boltonia vi
596	146	1	HBE_GALCR	P19759 galago cras	669	6	2.8	153	2	Q94L78	Q94lt8 oryza sativ
597	146	1	HBE_MACRU	P81042 macropus eu	670	6	2.8	153	2	Q8XDH3	Q8xdh3 escherichia
598	146	1	HBE_MICMU	Q28496 microcebus	671	6	2.8	153	2	Q7X127	Q7x127 oryza sativ
599	146	1	HBE_MOUSE	P02104 mus musculu	672	6	2.8	154	2	Q9SHG7	Q9shg7 arabidopsis
600	146	1	HBE_SMICR	Q28931 smnithopsis	673	6	2.8	155	2	Q14403	Q14403 homo sapien
601	146	1	HBG1_GORGO	P62741 gorilla gor	674	6	2.8	155	2	Q80312	Q80312 bacterioph
602	146	1	HBG1_HYLLA	P61948 hylobates l	675	6	2.8	155	2	Q93YA5	Q93ya5 bacillus ce
603	146	1	HBG1_PANPA	Q28779 pan paniscu	676	6	2.8	155	2	Q63EE2	Q63ee2 bacillus ce
604	146	1	HBG1_PANTR	P61920 pan troglod	677	6	2.8	155	2	Q8XPV4	Q8xpv4 ralstonia s
605	146	1	HBG1_PONPY	P18995 pongo pygma	678	6	2.8	155	2	Q6MRI9	Q6mri9 bdellovibri
606	146	1	HBG2_GORGO	P62742 gorilla gor	679	6	2.8	155	2	Q73BS3	Q73bs3 bacillus ce
607	146	1	HBG2_HYLLA	P61948 hylobates l	680	6	2.8	155	2	Q746S1	Q746s1 geobacter s
608	146	1	HBG2_PANTR	P61921 pan troglod	681	6	2.8	156	2	Q81GH8	Q81gh8 bacillus ce
609	146	1	HBG2_PONPY	P18996 pongo pygma	682	6	2.8	156	2	Q81TN3	Q81tn3 bacillus an
610	146	1	HBG_CHEME	P08224 cheirogaleu	683	6	2.8	156	2	Q6EEB1	Q6eeb1 protopterus
611	146	1	HBG_EULFU	P08225 eulemur ful	684	6	2.8	157	2	Q68SU5	Q68su5 pleurotus d
612	146	1	HBG_GALCR	P19760 galago cras	685	6	2.8	157	2	Q6ZUY2	Q6zuy2 homo sapien
613	146	1	HBG_HUMAN	P62027 homo sapien	686	6	2.8	157	2	Q8T013	Q8t013 drosophila
614	146	1	HBG_MACFU	P68078 macaca fusc	687	6	2.8	157	2	Q9LTK4	Q9ltk4 arabidopsis
615	146	1	HBG_MACMU	P68077 macaca mula	688	6	2.8	157	2	Q6HLV9	Q6hlv9 bacillus th



689	6	2.8	157	2	Q7ZZT8	Q7zzt8 oreochromis	762	6	2.8	176	2	Q8DHY0	Q8dhy0 synechococc
690	6	2.8	158	1	Y052_ARCFU	Q30184 archaeoglob	763	6	2.8	176	2	Q8ESG6	Q8esg6 shewanella
691	6	2.8	158	2	Q7SD90	Q7sd90 neurospora	764	6	2.8	177	2	Q7IS60	Q7is60 homo sapien
692	6	2.8	158	2	Q69ML0	Q69ml0 oryza sativ	765	6	2.8	177	2	Q9FQ99	Q9fg99 arabidopsis
693	6	2.8	158	2	Q9XC44	Q9xc44 methylococc	766	6	2.8	177	2	Q63HA4	Q63ha4 bacillus ce
694	6	2.8	158	2	Q7TWI3	Q7twi3 mycobacteri	767	6	2.8	177	2	Q73PB0	Q73fb0 bacillus ce
695	6	2.8	158	2	Q9KSB7	Q9ksb7 vibrio chol	768	6	2.8	177	2	Q81J54	Q81j54 bacillus ce
696	6	2.8	158	2	Q6PA17	Q6pal7 xenopus lae	769	6	2.8	177	2	Q81VU4	Q81vu4 bacillus an
697	6	2.8	159	2	Q9VA42	Q9va42 drosophila	770	6	2.8	177	2	Q8HPS2	Q8hps2 bacillus th
698	6	2.8	159	2	Q6TFX5	Q6tfx5 erwinia amy	771	6	2.8	177	2	Q6KYJ3	Q6kyj3 bacillus an
699	6	2.8	159	2	Q70G06	Q70g06 pseudomonas	772	6	2.8	178	1	LACB_BOVIN	P02754 bos taurus
700	6	2.8	159	2	Q8GFV4	Q8gfv4 citrobacter	773	6	2.8	178	2	Q7Q9E8	Q7q9e8 anopheles g
701	6	2.8	159	2	Q9EWQ9	Q9ewq9 streptomyce	774	6	2.8	178	2	Q84363	Q84363 chlamydia t
702	6	2.8	159	2	Q8BL68	Q8bl68 mus musculu	775	6	2.8	178	2	Q8EWG5	Q8ewg5 mycoplasma
703	6	2.8	159	2	Q75XW6	Q75xw6 fugu rubrip	776	6	2.8	179	1	FRIH_CHICK	P08267 gallus gall
704	6	2.8	160	1	ISPF_THETN	Q8r7s8 thermoanaer	777	6	2.8	179	2	Q6IGW9	Q6igw9 drosophila
705	6	2.8	160	2	Q7QAI0	Q7qai0 anopheles g	778	6	2.8	179	2	Q84KF3	Q84kf3 glycine max
706	6	2.8	160	2	Q46174	Q46174 clostridium	779	6	2.8	179	2	Q84IF3	Q84if3 selenomonas
707	6	2.8	160	2	Q89RK0	Q89rk0 bradyrhizob	780	6	2.8	179	2	Q8RGJ3	Q8rgj3 fusbobacteri
708	6	2.8	162	1	IL2_CEREL	P51747 cervus elap	781	6	2.8	180	1	FRIH_PIG	P19130 sus scrofa
709	6	2.8	162	1	LACB_OVIMU	P67975 ovis orient	782	6	2.8	180	1	LACB_BUBBU	P02755 bubalus bub
710	6	2.8	162	2	Q9UK75	Q9uk75 homo sapien	783	6	2.8	180	1	LACB_CAPHI	P02756 capra hircu
711	6	2.8	162	2	Q9MG88	Q9mg88 chrysodidym	784	6	2.8	180	1	LACB_SHEEP	P67976 ovis aries
712	6	2.8	162	2	Q7XI43	Q7xi43 oryza sativ	785	6	2.8	180	2	Q9HKQ7	Q9hkq7 thermoplasm
713	6	2.8	163	2	Q6ZVB8	Q6zvb8 homo sapien	786	6	2.8	180	2	Q96217	Q96217 dermatophag
714	6	2.8	163	2	Q7V890	Q7v890 prochloroco	787	6	2.8	180	2	Q6FE64	Q6fe64 acinetobact
715	6	2.8	164	1	FRIH_RABIT	P25915 oryctolagus	788	6	2.8	180	2	Q72LQ5	Q72lq5 thermus the
716	6	2.8	164	2	Q73N39	Q73n39 treponema d	789	6	2.8	181	1	APT2_YEAST	P36973 saccharomyc
717	6	2.8	165	2	Q8TD27	Q8td27 homo sapien	790	6	2.8	181	1	FRIH_MOUSE	P09528 mus musculu
718	6	2.8	165	2	Q9DFE9	Q9dfe9 oncorhynch	791	6	2.8	181	1	FRIH_RAT	P19132 rattus norv
719	6	2.8	166	1	RS5_BACAN	Q81vr3 bacillus an	792	6	2.8	181	2	Q7OK06	Q7ok06 anopheles g
720	6	2.8	166	2	Q8W700	Q8wx00 homo sapien	793	6	2.8	181	2	Q8RSP9	Q8rsp9 rhizobium l
721	6	2.8	166	2	Q9L2P2	Q9l2p2 arabidopsis	794	6	2.8	181	2	Q6REG9	Q6reg9 rhodococcus
722	6	2.8	166	2	Q63H73	Q63h73 bacillus ce	795	6	2.8	181	2	Q6PRV1	Q6prv1 coturnix co
723	6	2.8	166	2	Q73F79	Q73f79 bacillus ce	796	6	2.8	182	1	FRIH_HUMAN	P02794 homo sapien
724	6	2.8	166	2	Q6HPP1	Q6hpp1 bacillus th	797	6	2.8	182	1	FRIH_TRIVU	Q9xt73 trichosurus
725	6	2.8	166	2	Q9Q5L0	Q9q5l0 herpesvirus	798	6	2.8	182	2	Q6UWJ5	Q6uwj5 homo sapien
726	6	2.8	167	1	RS5_BACCR	Q81j25 bacillus ce	799	6	2.8	182	2	Q9H7Y0	Q9h7y0 homo sapien
727	6	2.8	167	2	Q7MRZ1	Q7mr11 wolinnella s	800	6	2.8	182	2	Q8MIP0	Q8mip0 equus cabal
728	6	2.8	168	2	Q9Y820	Q9y820 aeropyrum p	801	6	2.8	182	2	Q8GA64	Q8ga64 escherichia
729	6	2.8	168	2	Q6BW24	Q6bw24 debaryomyce	802	6	2.8	182	2	Q8XUF6	Q8xuf6 ralatonia s
730	6	2.8	168	2	Q81GP0	Q81gp0 drosophila	803	6	2.8	182	2	Q836K0	Q836k0 enterococcu
731	6	2.8	168	2	Q7RNS8	Q7rns8 plasmodium	804	6	2.8	182	2	Q92OK4	Q92ok4 cavia porce
732	6	2.8	168	2	Q6R4W3	Q6r4w3 bacterioph	805	6	2.8	182	2	Q9CUG0	Q9cug0 mus musculu
733	6	2.8	168	2	Q6LAF5	Q6laf5 mus musculu	806	6	2.8	183	1	PSAF_GUITH	Q78457 guillardia
734	6	2.8	168	2	Q9JE54	Q9je54 human immu	807	6	2.8	183	2	Q6NZ44	Q6nz44 homo sapien
735	6	2.8	169	2	Q7QV07	Q7qv07 giardia lam	808	6	2.8	183	2	Q6BFK4	Q6bfk4 paramecium
736	6	2.8	169	2	Q9RV50	Q9rv50 deinococcus	809	6	2.8	183	2	Q95MP7	Q95mp7 canis fami
737	6	2.8	169	2	Q9RWJ6	Q9rwj6 deinococcus	810	6	2.8	183	2	Q94BT7	Q94bt7 arabidopsis
738	6	2.8	169	2	Q9JE79	Q9je79 human immu	811	6	2.8	183	2	Q6ZHP7	Q6zhp7 oryza sativ
739	6	2.8	170	2	Q7Q086	Q7q086 anopheles g	812	6	2.8	183	2	Q9LI88	Q9li88 arabidopsis
740	6	2.8	170	2	Q947M1	Q947m1 beta vulgar	813	6	2.8	184	2	Q9YCI3	Q9yci3 aeropyrum p
741	6	2.8	170	2	Q84182	Q84182 chlamydia t	814	6	2.8	184	2	Q7QFJ4	Q7qfj4 anopheles g
742	6	2.8	171	2	Q68SU3	Q68su3 pleurotus d	815	6	2.8	184	2	Q9XSG6	Q9xsg6 bos taurus
743	6	2.8	171	2	Q68SU8	Q68su8 pleurotus d	816	6	2.8	184	2	Q98PS7	Q98ps7 mycoplasma
744	6	2.8	171	2	Q81BA7	Q81ba7 bacillus ce	817	6	2.8	184	2	Q830W2	Q830w2 enterococcu
745	6	2.8	171	2	Q9J5E3	Q9j5e3 human immu	818	6	2.8	184	2	Q640C7	Q640c7 xenopus lae
746	6	2.8	172	2	Q81L05	Q81l05 plasmodium	819	6	2.8	185	1	FRIH_CRIGR	P29389 cricetulus
747	6	2.8	172	2	Q6IL45	Q6ilas drosophila	820	6	2.8	186	1	APL3_GALME	P80703 gallieria me
748	6	2.8	172	2	Q8LIW6	Q8liw6 oryza sativ	821	6	2.8	186	1	THM2_ARATH	Q9seu8 arabidopsis
749	6	2.8	172	2	Q6MCT6	Q6mct6 parachlamyd	822	6	2.8	186	2	Q8ZUQ9	Q8zuz9 pyrobaculum
750	6	2.8	172	2	Q03457	Q03457 feline leuk	823	6	2.8	186	2	Q8LG26	Q8lg26 arabidopsis
751	6	2.8	173	2	Q9B8U8	Q9b8u8 schistosoma	824	6	2.8	186	2	Q6NTR3	Q6ntr3 xenopus lae
752	6	2.8	173	2	Q7ME16	Q7me16 vibrio vuln	825	6	2.8	187	2	Q702D9	Q702d9 uncultured
753	6	2.8	173	2	Q8D3X9	Q8d3x9 vibrio vuln	826	6	2.8	187	2	Q68IJ9	Q68ij9 helicobacte
754	6	2.8	173	2	Q9A9B1	Q9a9b1 caulobacter	827	6	2.8	187	2	Q68IJ1	Q68ij1 helicobacte
755	6	2.8	174	1	PH4A_ARATH	Q84tf5 arabidopsis	828	6	2.8	187	2	Q68IJ2	Q68ij2 helicobacte
756	6	2.8	174	2	Q85594	Q85594 human t-lym	829	6	2.8	187	2	Q68IJ7	Q68ij7 helicobacte
757	6	2.8	176	2	Q81755	Q81755 plasmodium	830	6	2.8	187	2	Q68IJ8	Q68ij8 helicobacte
758	6	2.8	176	2	Q7RK79	Q7rk79 plasmodium	831	6	2.8	187	2	Q68IJ9	Q68ij9 helicobacte
759	6	2.8	176	2	Q7XM27	Q7xm27 oryza sativ	832	6	2.8	187	2	Q68IK0	Q68ik0 helicobacte
760	6	2.8	176	2	Q81H78	Q81h78 bacillus ce	833	6	2.8	187	2	Q68IK1	Q68ik1 helicobacte
761	6	2.8	176	2	Q89TC0	Q89tc0 bradyrhizob	834	6	2.8	187	2	Q68IK2	Q68ik2 helicobacte

835	187	2	681K3	Q68iK3 helicobacte	908	2.8	201	2	Q8Y2R2	Q8Y2r2 ralstonia s
836	187	2	Q68IK4	Q68iK4 helicobacte	909	2.8	201	2	Q8RFH0	Q8rfh0 rhizobium l
837	187	2	Q68IK5	Q68iK5 helicobacte	910	2.8	202	1	RR4_NEPOL	Q8tkx5 nephroselm
838	187	2	Q68IK6	Q68iK6 helicobacte	911	2.8	202	2	Q64A84	Q64a84 uncultured
839	187	2	Q68IK7	Q68iK7 helicobacte	912	2.8	202	2	Q66I49	Q66i49 homo sapien
840	187	2	Q68IK9	Q68iK9 helicobacte	913	2.8	202	2	Q6AUX7	Q6aux7 oryza sativ
841	187	2	Q68IL0	Q68iL0 helicobacte	914	2.8	202	2	Q6LR08	Q6lr08 photobacter
842	187	2	Q68IL1	Q68iL1 helicobacte	915	2.8	202	2	Q83GI4	Q83gi4 tropheryma
843	187	2	Q68IL2	Q68iL2 helicobacte	916	2.8	202	2	Q83HP6	Q83hp6 tropheryma
844	187	2	Q68IL5	Q68iL5 helicobacte	917	2.8	202	2	Q9S2G6	Q9s2g6 streptomyce
845	187	2	Q68IL6	Q68iL6 helicobacte	918	2.8	202	2	Q82444	Q82444 human t-lym
846	187	2	Q68IL7	Q68iL7 helicobacte	919	2.8	203	2	Q6R2R2	Q6r2r2 pan troglod
847	187	2	Q68IL8	Q68iL8 helicobacte	920	2.8	203	2	Q6EPW8	Q6epw8 oryza sativ
848	187	2	Q68IL9	Q68iL9 helicobacte	921	2.8	204	1	ALA7_ALTAL	P42058 alternaria
849	187	2	Q68IM1	Q68iM1 helicobacte	922	2.8	204	1	CTF2_MOUSE	P83714 mus musculu
850	187	2	Q68IM4	Q68iM4 helicobacte	923	2.8	204	2	Q8STS1	Q8stsl encephalito
851	187	2	Q68IM6	Q68iM6 helicobacte	924	2.8	204	2	Q7XRT5	Q7xrt5 oryza sativ
852	187	2	Q68IM7	Q68iM7 helicobacte	925	2.8	204	2	Q88IW7	Q88iw7 pseudomonas
853	187	2	Q68IM8	Q68iM8 helicobacte	926	2.8	204	2	Q6R2R3	Q6r2r3 rattus norv
854	187	2	Q68IN0	Q68iN0 helicobacte	927	2.8	205	2	Q7Z2I8	Q7z2i8 homo sapien
855	188	1	RNFB_YERPE	Q8zec9 versinia pe	928	2.8	205	2	Q45046	Q45046 scirpophaga
856	188	2	Q6Z8F2	Q6z8f2 oryza sativ	929	2.8	205	2	Q86AW1	Q86aw1 dictyosteli
857	188	2	Q8P9N4	Q8p9n4 xanthomonas	930	2.8	205	2	Q6F909	Q6f909 acinetobact
858	188	2	Q8PLG1	Q8plg1 xanthomonas	931	2.8	205	2	Q8KI75	Q8ki75 mus musculu
859	188	2	Q882W8	Q882w8 pseudomonas	932	2.8	206	1	PTH_PROMM	Q7v4v4 prochloroco
860	189	2	Q9CAM2	Q9cam2 arabidopsis	933	2.8	206	2	Q8RNX5	Q8rnx5 serratia sp
861	190	2	Q26019	Q26019 helicobacte	934	2.8	207	2	Q66AG4	Q66ag4 versinia ps
862	190	2	Q9ZJD4	Q9zjd4 helicobacte	935	2.8	207	2	Q9HX32	Q9hx32 pseudomonas
863	191	2	Q8RSI4	Q8rsi4 uncultured	936	2.8	208	2	Q21506	Q21506 meriones un
864	191	2	Q9QCX2	Q9qcX2 chayote mos	937	2.8	208	2	Q9FLJ1	Q9flj1 arabidopsis
865	192	1	RM11_HUMAN	Q9y3b7 homo sapien	938	2.8	208	2	Q69L68	Q69l68 oryza sativ
866	192	1	RM11_MOUSE	Q9c9f0 mus musculu	939	2.8	208	2	Q8XYN2	Q8xyn2 ralstonia s
867	192	2	Q74N68	Q74n68 nanoarchaeu	940	2.8	208	2	Q7MH18	Q7mh18 vibrio vuln
868	192	2	Q9FU09	Q9fuq9 oryza mayer	941	2.8	208	2	Q8DCC1	Q8dcl1 vibrio vuln
869	193	2	Q6ZSX6	Q6zSX6 homo sapien	942	2.8	209	2	Q9ZV79	Q9zv79 arabidopsis
870	193	2	Q85MC2	Q85mc2 monoblephar	943	2.8	209	2	Q930U4	Q930u4 rhizobium m
871	193	2	Q8H7G4	Q8h7g4 arabidopsis	944	2.8	209	2	Q68VN7	Q68vn7 rickettsia
872	193	2	Q93J01	Q93j01 streptomyce	945	2.8	210	2	Q9BSE9	Q9bse9 homo sapien
873	194	2	Q6ZNG4	Q6zng4 homo sapien	946	2.8	210	2	Q8MRP3	Q8mrp3 drosophila
874	194	2	Q93YL3	Q93yl3 brassica na	947	2.8	210	2	Q84BA4	Q84ba4 erwinia chr
875	194	2	Q7VB03	Q7vb03 prochloroco	948	2.8	210	2	Q8DXS1	Q8dxsl streptococc
876	194	2	Q6ARI1	Q6aril desulfotale	949	2.8	210	2	Q8E3E1	Q8e3e1 streptococc
877	194	2	Q6HIK8	Q6hiK8 bacillus th	950	2.8	210	2	Q8EGU9	Q8eg9 shewanella
878	195	2	Q6BYJ1	Q6byj1 debaryomyce	951	2.8	211	1	RL4_TREDE	P61070 treponema d
879	195	2	Q72M47	Q72m47 leptospira	952	2.8	211	2	Q6ZQZ3	Q6zqz3 homo sapien
880	195	2	Q8EYM4	Q8eym4 leptospira	953	2.8	211	2	Q7LDF1	Q7ldf1 drosophila
881	196	2	Q9VKF5	Q9vKf5 drosophila	954	2.8	211	2	Q7PM91	Q7pm91 anopheles g
882	196	2	Q7MMW3	Q7mmw3 vibrio vuln	955	2.8	211	2	Q95K58	Q95k58 macaca fasc
883	196	2	Q87SH6	Q87sh6 vibrio para	956	2.8	211	2	Q9FYZ7	Q9fyz7 nicotiana t
884	196	2	Q8DEJ7	Q8dej7 vibrio vuln	957	2.8	211	2	Q6RGN7	Q6rgn7 streptomyce
885	197	1	CYCL_BACSU	Q34577 bacillus su	958	2.8	211	2	Q7NZV7	Q7nzy7 chromobacte
886	197	2	Q6CG00	Q6c900 yarrowia li	959	2.8	211	2	Q81QC1	Q81qc1 bacillus an
887	197	2	Q6NUU2	Q6nuj2 homo sapien	960	2.8	212	1	FSAD_SPIOL	P12353 spinacia ol
888	197	2	Q6XU46	Q6xi46 drosophila	961	2.8	212	2	Q7SGR9	Q7sgr9 neurospora
889	197	2	Q8HY68	Q8hy68 macropus fu	962	2.8	212	2	Q04646	Q04646 arabidopsis
890	197	2	Q9ST13	Q9st13 brassica ca	963	2.8	212	2	Q8LD12	Q8ld12 arabidopsis
891	197	2	Q93L53	Q93l53 bacteroides	964	2.8	212	2	Q9XH35	Q9xh35 oryza sativ
892	197	2	Q6G4S4	Q6g4s4 bartonella	965	2.8	212	2	Q7P2A5	Q7p2a5 fusobacteri
893	197	2	Q7NJA3	Q7nja3 gloeobacter	966	2.8	212	2	Q8RFQ2	Q8rfq2 fusobacteri
894	197	2	Q6NXW2	Q6nxw2 mus musculu	967	2.8	212	2	Q74CQ2	Q74cq2 geobacter s
895	197	2	Q6P9V2	Q6p9v2 rattus norv	968	2.8	212	2	Q884R0	Q884r0 pseudomonas
896	198	2	Q9Y3V6	Q9y3v6 homo sapien	969	2.8	212	2	Q89R64	Q89r64 bradyrhizob
897	198	2	Q6MAP7	Q6map7 parachlamyd	970	2.8	212	2	Q9FL33	Q9fl33 pseudomonas
898	199	1	SP25_DROME	Q9vy72 drosophila	971	2.8	214	2	Q92R50	Q92r50 rhizobium m
899	199	2	Q6GOK5	Q6gok5 bartonella	972	2.8	215	2	Q635I8	Q635i8 bacillus ce
900	200	1	TRPG_BUCAI	Q44696 buchnera ap	973	2.8	215	2	Q92YY9	Q92yy9 rhizobium m
901	200	2	Q7SGU7	Q7sgu7 neurospora	974	2.8	215	2	Q73IK5	Q73ik5 bacillus ce
902	200	2	Q81308	Q81308 arabidopsis	975	2.8	215	2	Q818Z4	Q818z4 bacillus ce
903	200	2	Q65HV0	Q65hv0 bacillus li	976	2.8	215	2	Q81MD5	Q81md5 bacillus an
904	201	2	Q8MQ07	Q8mq07 caenorhabdi	977	2.8	215	2	Q6HE74	Q6he74 bacillus th
905	201	2	Q6ZG76	Q6zg76 oryza sativ	978	2.8	216	1	YD82_RHIME	Q9zqeb rhizobium m
906	201	2	Q7XBK0	Q7xbk0 papaver nud	979	2.8	216	2	Q6BFR2	Q6bfr2 paramecium
907	201	2	Q25881	Q25881 helicobacte	980	2.8	216	2	Q9N208	Q9n208 callithrix

981	6	2.8	216	2	Q64YM8	Q64ym8 bacteroides
982	6	2.8	216	2	G6ACN6	Q6acn6 leifsonia x
983	6	2.8	216	2	G809H7	Q809h7 influenza a
984	6	2.8	216	2	Q809H8	Q809h8 influenza a
985	6	2.8	216	2	Q809H9	Q809h9 influenza a
986	6	2.8	216	2	Q809I0	Q809i0 influenza a
987	6	2.8	216	2	Q809I1	Q809i1 influenza a
988	6	2.8	216	2	Q809I2	Q809i2 influenza a
989	6	2.8	216	2	Q809I3	Q809i3 influenza a
990	6	2.8	216	2	Q809I4	Q809i4 influenza a
991	6	2.8	216	2	Q809I5	Q809i5 influenza a
992	6	2.8	216	2	Q809I6	Q809i6 influenza a
993	6	2.8	216	2	Q809I7	Q809i7 influenza a
994	6	2.8	216	2	Q809I8	Q809i8 influenza a
995	6	2.8	216	2	Q809I9	Q809i9 influenza a
996	6	2.8	216	2	Q809J0	Q809j0 influenza a
997	6	2.8	216	2	Q809J1	Q809j1 influenza a
998	6	2.8	216	2	Q809J2	Q809j2 influenza a
999	6	2.8	216	2	Q809J3	Q809j3 influenza a
1000	6	2.8	216	2	Q809J4	Q809j4 influenza a

## ALIGNMENTS

## RESULT 1

AC 11F7 HUMAN STANDARD; PRT; 218 AA.  
AD Q9NHG6; Q9TD04; Q9TD05; Q9HBF2; Q9HBF3; Q9UHA6;  
AC Q9NHG6; Q9TD04; Q9TD05; Q9HBF2; Q9HBF3; Q9UHA6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin 1 family member 7 precursor (IL1-F7) (Interleukin-1 zeta)  
DE (IL-1 zeta) (Fili zeta) (interleukin-1 homolog 4) (IL-1H4)  
DE (Interleukin-1-related protein) (IL-1RP1) (IL-1X protein).  
GN Names:IL1F7; Synonyms:IL1Z, IL1H4, IL1RP1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxId=9606;  
RN [1]  
RN SEQUENCE FROM N.A. (ISOFORM B).  
RP TISSUE=Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;  
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
RA young P.R.;  
RT "Identification and initial characterization of four novel members of  
RT the interleukin-1 family.";  
RL J. Biol. Chem. 275:10308-10314(2000).

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MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
RA S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
RA "Genomic organization of the interleukin-1 locus.";
RL Genomics 79:726-733(2002).
[6]
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ALA-42.
RN TISSUE=Placenta;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.C., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds to interleukin-18 receptor (IL-18R) receptor but
CC not to IL-1 receptor. Could be a new player in the inflammatory
CC and immune responses mediated by the IL-18/IL-18R axis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=B;
CC IsoId=Q9NZH6-1; Sequence=Displayed;
CC Name=A;
CC IsoId=Q9NZH6-2; Sequence=VSP_002653;
CC Name=C;
CC IsoId=Q9NZH6-3; Sequence=VSP_002656;
CC Name=D;
CC IsoId=Q9NZH6-4; Sequence=VSP_002654;
CC Name=E;
CC IsoId=Q9NZH6-5; Sequence=VSP_002655;
CC -!- TISSUE SPECIFICITY: Isoforms A_ B and C are expressed in testis,
CC colon, placenta, lung and lymph node. Isoforms D and E were found
CC only in testis and bone marrow. Whereas only isoform A is found in
CC brain, only isoform B in kidney and only isoform C in heart.
CC -!- INDUCTION: By phorbol ester (PMA) in different cell lines.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; AF200496; AAF69252.1; -
CC ENBL; AF167368; AAG29344.1; -
CC ENBL; AF251118; AAG14420.1; -
CC ENBL; AF251120; AAG14422.1; -
CC ENBL; AF251119; AAG14421.1; -
CC ENBL; AF201832; AAF25212.1; -
CC ENBL; AY071840; AAL67151.1; -
CC ENBL; AY071841; AAL67154.1; -
CC ENBL; BC020637; AAH20637.1; -
CC HSPSP; P18510; IL1R.
CC Genew; HGNC:15563; IL1F7.
CC H-InVDB; HIX0002387; -
CC MIM; 605510; -
CC GO; GO:0005576; C:extracellular; TAS.

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DR GO: 0005149; F:interleukin-1 receptor binding; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro; IPR008996; Cytok IL1 like.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00253; Interleukin_1; 1.
DR PROSITE; PS00253; INTERLEUKIN 1; FALSE NEG.
KW Alternative splicing; Cytokine; Direct protein sequencing;
KW Multigene family; Polymorphism.
FT PROPEP 1 45 Removed in mature form.
FT CHAIN 46 218 Interleukin 1 family member 7.
FT VARSPLIC 1 49 MSFVGENSGVMGSEDEKDEPQCLEDPAQSPLPQPSLP
FT TMNFVHTS -> MSGCDRRETETKGNFKKRLRG (in isoform A)
FT FTid=VSP_002653.
FT DPAGSPLPGLPSLTMMNFVHTS -> G (in isoform D).
FT VARSPLIC 28 49 /FTid=VSP_002654.
FT VARSPLIC 28 88 Missing (in isoform E).
FT VARSPLIC 49 89 /FTid=VSP_002655.
FT VARSPLIC 49 89 SPKYNLNPFKFSHDQHKVLVDGSLIAVPDKNVIRPE
FT -> K (in isoform C).
FT VARIANT 31 31 /FTid=VSP_002656.
FT VARIANT 42 42 /FTid=VAR_014260.
FT VARIANT 42 42 T -> A.
FT SEQUENCE 218 AA; 24126 MW; 96E089310D2CEA68 CRC64;
Query Match 80.7%; Score 176; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.6e-172;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 43 MNFVHTSPKYNLNPFKFSHDQHKVLVDGSLIAVPDKNVIRPIFFALASLSAS 102
Db 43 MNFVHTSPKYNLNPFKFSHDQHKVLVDGSLIAVPDKNVIRPIFFALASLSAS 102
Qy 103 AEKGSPIILGVSGEFLCYCDKDGQSHPSLQKELKMLAAQKESARRPFIFRAQVG 162
Db 103 AEKGSPIILGVSGEFLCYCDKDGQSHPSLQKELKMLAAQKESARRPFIFRAQVG 162
Qy 163 SNNMLESAAHPGWICTSCNPNVGVTDKFNKHIIEFSFPYCKAEMPSEVSD 218
Db 163 SNNMLESAAHPGWICTSCNPNVGVTDKFNKHIIEFSFPYCKAEMPSEVSD 218
RESULT 2
Q7RU00 PRELIMINARY; PRT; 219 AA.
AC Q7RU00
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IL-1F7b (IL-1H4, IL-1H, IL-1RP1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545212; PubMed=11093146;
RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.J.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
RA Northwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
RA Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,

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RA Hildebrandt F.;
RT "Molecular cloning of the interleukin-1 gene cluster: construction of
an integrated YAC/PAC contig and a partial transcriptional map in the
region of chromosome 2q13.";
RL Genomics 41:370-378(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245215; PubMed=8188271;
RX Nicklin M.J.H., Weith A., Duff G.W.;
RT "A Physical map of the region encompassing the human interleukin-1-
alpha, interleukin-1-beta and interleukin-1 receptor genes.";
RL Genomics 19:382-384(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=2198050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
RX Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
RX Kornman K.;
RT "A sequence-based map of the nine genes of the human interleukin-1
cluster.";
RL Genomics 79:718-725(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
RX Mulero J.J., Pace A.M., Neiken S.T., Loeb D.D., Correa T.R.,
RX Drmanac R., Ford J.E.;
RT "IL1H1: A novel interleukin-1 receptor antagonist gene.";
RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
RX Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RX Sims J.E.;
RT "Four new members expand the interleukin-1 superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RX Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RX Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RX Young P.R.;
RT "Identification and initial characterization of four novel members of
the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
RX Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RX Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the
IL-1 family on human chromosome 2.";
RL Genomics 66:213-216(2000).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
RX Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RX Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vanden R.;
RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
1krp.";
RL Cytokine 13:1-7(2001).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
RX Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
RX Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT "Cloning and characterization of IL-1H2, a novel interleukin-1 family
member.";
RL J. Biol. Chem. 276:20597-20602(2001).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359532; PubMed=11466363;
RX Debets R., Timans J.C., Honey B., Zurawski S., Sana T.R., Lo S.,
RX Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RX Kastelein R.A.;

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RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function  
as an antagonist and agonist of NF-kB activation through the orphan  
IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";  
RL J. Immunol. 167:1440-1446(2001).  
RN [12]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;  
RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,  
Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G.,  
Pan Y., Smith D.E., Young P.R.;  
RT "A new nomenclature for the IL-1-family genes.";  
RL Trends Immunol. 22:536-537(2001).  
CC -1- MISCELLANEOUS: The sequence shown here is derived from an  
EMBL/GenBank/DBJ third party annotation (TPA) entry.  
CC -1- SIMILARITY: Belongs to the IL-1 family.  
DR EMBL; BN000002; CAD29873.1; -.  
DR HSSP; Q9QY1; 1MD6.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; Cyto\_kinlike.  
DR InterPro; IPR003297; InterleukinIL1RA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR PRINTS; PR00264; INTERLEUKIN1.  
DR PRINTS; PR01360; INTRLEUKIN1X.  
DR ProDom; PD002536; Interleukin\_1; 1.  
SQ SEQUENCE 219 AA; 24242 MW; 18EBA0881DF25C41 CRC64;  
  
Query Match 25.2%; Score 55; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 7e-48;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 109 ILLGVSKGEFLCYCDKQGSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGS 163  
DB 109 ILLGVSKGEFLCYCDKQGSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGS 163  
  
RESULT 3  
Q97CB6 ID Q97CB6 PRELIMINARY; PRT; 196 AA.  
AC Q97CB6  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein TVG0192051.  
GN Names=TVG0192051; OrderedLocusNames=TV0186;  
OS Thermoplasma volcanium.  
OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmatales;  
OC Thermoplasmataceae; Thermoplasma.  
OX NCBI\_TaxID=50339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=GSS1 / DSM 4299 / JCM 9571;  
RL MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;  
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,  
Kawashima T., Watanabe S., Yamazaki M., Kanehori K., Kawamoto T.,  
Nunohiwa T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;  
RT "Archaeal adaptation to higher temperatures revealed by genomic  
sequence of Thermoplasma volcanium.";  
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).  
RL EMBL; AP000991; BAB59328.1; -.  
DR HSSP; Q9X033; 1O50.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR000644; CBS.  
DR InterPro; IPR001387; HTH\_3.  
DR InterPro; IPR010982; Lambda\_like\_DNA.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF01381; HTH\_3; 1.  
DR SMART; SM00116; CBS; 2.  
DR SMART; SM00530; HTH\_XRE; 1.  
DR PROSITE; PS00943; HTH\_CROCI; 1.  
KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 196 AA; 21798 MW; 41132CC5DBBC3CDC CRC64;  
  
Query Match 4.1%; Score 9; DB 2; Length 196;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 69 VLVLDSGNL 77  
DB 171 VLVLDSGNL 179  
  
RESULT 4  
Q9SAQ1 ID Q9SAQ1 PRELIMINARY; PRT; 97 AA.  
AC Q9SAQ1  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MRP-like ABC transporter (Fragment).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97415407; PubMed=9271206; DOI=10.1016/S0014-5793(97)00702-3;  
RA Tommasini R., Vogt E., Schmid J., Fromentau M., Amrhein N.,  
RA Martinoia E.;  
RT "Differential expression of genes coding for ABC transporters after  
treatment of Arabidopsis thaliana with xenobiotics.";  
FEBS Lett. 411:206-210(1997).  
DR EMBL; U96398; AAC49796.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR003439; ABC\_transporter.  
DR ProDom; PD000006; ABC\_transporter; 1.  
FT NON\_TER 1  
FT NON\_TER 97  
SQ SEQUENCE 97 AA; 10774 MW; 80971A33465B2D33 CRC64;  
  
Query Match 3.7%; Score 8; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 68 KVLVLDSG 75  
DB 51 KVLVLDSG 58  
  
RESULT 5  
Q6ZQY2 ID Q6ZQY2 PRELIMINARY; PRT; 161 AA.  
AC Q6ZQY2  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein FLJ46805.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=trachea;  
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,  
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,  
Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,  
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

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RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK128646; BAC87547.1; -.
DR InterPro; IPR003590; LRR_RNinh_sub.
DR SMART; SM00368; LRR_R1; 2.
SQ SEQUENCE 161 AA; 17279 MW;  C4643C22000F493 CRC64;

Query Match          3.7%; Score 8; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100
Db 98 ALASSLS 105
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RESULT 6
Q87JK9 PRELIMINARY; PRT; 234 AA.
AC Q87JK9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative repressor protein PhnR.
GN OrderedLocusNames=VPA0240;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIND 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nishima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
CC -1- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
DR EMBL; AP005084; BAC61583.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000524; HTH_GntR
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00392; GntR; 1.
DR PRINTS; PR00035; HTHGNTR.
DR SMART; SM00345; HTH_GNTR; 1.
DR PROSITE; PS50949; HTH_GNTR; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 234 AA; 27058 MW; 55AF101D68418E9C CRC64;

Query Match          3.7%; Score 8; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 NYIRPEIF 91
Db 138 NYIRPEIF 145
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RESULT 7
ID Q72ME6 PRELIMINARY; PRT; 256 AA.
AC Q72ME6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Response regulator.
GN OrderedLocusNames=IIC13242;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar

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OS Copenhageni).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fluctruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorzy H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172 (2004).
DR EMBL; AE017300; AAS71786.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR011006; CheY like.
DR InterPro; IPR011789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.
DR PRODOM; PD000039; Response_reg; 2.
DR SMART; SM00448; REC; 2.
DR PROSITE; PS50110; RESPONSE REGULATORY; 2.
KW Complete proteome; Phosphorylation; Sensory transduction.
SQ SEQUENCE 256 AA; 29077 MW; A3A28732218B146B CRC64;

Query Match          3.7%; Score 8; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLDSS 75
Db 2 KVLVLDSS 9
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RESULT 8
Q8EY26 PRELIMINARY; PRT; 256 AA.
ID Q8EY26
AC Q8EY26;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Two-component response regulator.
GN OrderedLocusNames=LA4065;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893 (2003).
DR EMBL; AE011561; AAN51263.1; -.
DR HSSP; Q9A514; 1MB3.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.

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DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR011006; Chef_like.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 2.
DR ProDom; PD0000039; Response_reg; 2.
DR SMART; SM00448; REC; 2.
DR PROSITE; PS01110; RESPONSE REGULATORY; 2.
KW Complete proteome; Phosphorylation; Sensory transduction.
SQ SEQUENCE 256 AA; 29104 MW; 3f4f972f280dc689 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 KVLVLD SG 75
Db 2 KVLVLD SG 9

RESULT 9
ID 073909 PRELIMINARY; PRT; 267 AA.
AC 073909;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-1beta.
GN Names:il-1beta; Synonyms:IL1B;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archoaauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99144128; PubMed=9990317;
RA Weining K.C., Sick C., Kaspers B., Staeheli P.;
RT "A chicken homologue of mammalian interleukin-1beta: cDNA cloning and
RT purification of active recombinant protein.";
RL Eur. J. Biochem. 258:994-1000(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=line N;
RA Kaiser P., Rothwell L., Goodchild M., Bumstead N.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Produced by activated macrophages, IL-1 stimulates
CC thymocyte proliferation by inducing IL-2 release, B-cell
CC maturation and proliferation, and fibroblast growth factor
CC activity (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the IL-1 family.
DR EMBL; Y15006; CAA75239.1; -.
DR EMBL; AJ245728; CAC04510.1; -.
DR HSP; P18510; IL1R.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR008996; Cytok_IL1-like.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR003294; InterleukinIL1AB.
DR InterPro; IPR003296; InterleukinIL1B.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF02394; IL1; 1
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.
DR PRINTS; PR01357; INTRLEUKIN1AB.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.

DR PROSITE; PS00253; INTERLEUKIN 1; 1.
KW Inflammatory response; Mitogen; Pyrogen.
FT CHAIN 106 267 interleukin-1beta.
SQ SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 PGWFICT 180
Db 234 PGWFICT 241

RESULT 10
LPSL_RHIME STANDARD; PRT; 341 AA.
ID LPSL_RHIME
AC 054067;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UDP-glucuronate 5'-epimerase (EC 5.1.3.12) (UDP-glucuronic acid
DE epimerase).
GN Name:lspL; OrderedLocNames=R01083; ORFNames=SMC02640;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98440435; PubMed=9765575;
RA Kereszt A., Kiss E., Reuhs B.L., Carlson R.W., Kondorosi A.,
RA Putnoky P.;
RT "Novel rkp gene clusters of Sinorhizobium meliloti involved in
RT capsular polysaccharide production and invasion of the symbiotic
RT nodule: the rkp gene encodes a UDP-glucose dehydrogenase.";
RL J. Bacteriol. 180:5426-5431(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portecelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- CATALYTIC ACTIVITY: UDP-D-glucuronate = UDP-L-iduronate.
CC -1- COFACTOR: NAD.
CC -1- SIMILARITY: Belongs to the sugar epimerase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; A222861; CAA10917.1; -.
DR EMBL; AL591786; CAC45662.1; -.
DR PIR; T46572; T46572.
DR InterPro; IPR001509; Epimerase Dh.
DR InterPro; IPR008089; Nuc_sugar_epim.
DR Pfam; PF01370; Epimerase_1.
DR PRINTS; PR01713; NUCEPIMERASE.
KW Complete proteome; Isomerase; NAD.
FT CONFLICT 176 176 S -> A (in Ref. 1).
SQ SEQUENCE 341 AA; 38098 MW; D678ED2EAFD89395 CRC64;

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Query Match 3.7%; Score 8; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 VGSNNMLE 168
Db 105 VGSNNMLE 112

RESULT 11
PDK4 MOUSE
ID PDK4_MOUSE STANDARD; PRT; 412 AA.
AC 070571;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE [Pyruvate dehydrogenase (lipoamide)] kinase isozyme 4, mitochondrial
DE precursor (EC 2.7.1.99) (Pyruvate dehydrogenase kinase isoform 4).
GN Name=Pdk4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H; TISSUE=Heart;
RA Horiuchi M., Kobayashi K., Masuda M., Saheki T.;
RT "A novel gene in carnitine-deficient JVS mice";
RL Submitted (SEP-1997) to the ENBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Jeoung N.H., Bowker-Kinley M.M., Harris R.A.;
RT "Promoter and partial structural region of Mus musculus pyruvate
dehydrogenase kinase 4 (PDK4).";
RL Submitted (FEB-2000) to the ENBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Inhibits the mitochondrial pyruvate dehydrogenase
complex by phosphorylation of the E1 alpha subunit, thus
contributing to the regulation of glucose metabolism (By
similarity).
CC -!- CATALYTIC ACTIVITY: ATP + [pyruvate dehydrogenase (lipoamide)] =
ADP + [pyruvate dehydrogenase (lipoamide)] phosphate.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the PK/CKDK protein kinase family.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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QY 94 LASSLSA 101
Db 12 LASSLSA 19

RESULT 13
Q9UEU4 PRELIMINARY; PRT; 595 AA.
AC Q9UEU4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inidazoline receptor antisera-selected protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99066883; PubMed=9851558; DOI=10.1016/S0165-1838(98)00094-0;
RA Ivanov T.R., Jones J.C., Döntenwill M., Bousquet P., Pillet J.E.;
RT "Characterization of a partial cDNA clone detected by imidazoline
RT receptor-selective antisera.";
RL J. Auton. Nerv. Syst. 72:98-110(1998).
DR EMBL: AF058290; AAC33321.1; -.
DR GO: GO:0004872; P:receptor activity; IEA.
DR InterPro: IPR001128; CYTOCHROME_P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 595
FT NON_TER 595
FT NON_TER 595
SQ SEQUENCE 595 AA; 65354 MW; 93139B536F447C8D CRC64;

Query Match 3.7%; Score 8; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 ALASSLS 100
Db 50 ALASSLS 57

RESULT 14
Q8RX76 PRELIMINARY; PRT; 787 AA.
AC Q8RX76
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE A1930400/T4K22.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL: AY090258; AAL90919.1; -.
DR HSP; Q9CHL6; LMV5.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.

GO: GO:0006810; P:transport; IEA.
InterPro: IPR003593; AAA_ATPase.
InterPro: IPR011527; ABC_membrane_1.
InterPro: IPR011140; ABC_TM_transp.
InterPro: IPR003439; ABC_transporter.
Pfam: PF00664; ABC_membrane; 1.
Pfam: PF00005; ABC_tran; 1.
ProDom: PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
DR PROSITE; PS00929; ABC_TMIF; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding.
SQ SEQUENCE 787 AA; 87774 MW; 4D3532D4BAADD469 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 KVLVLD 75
Db 605 KVLVLD 612

RESULT 15
Q7SE30 PRELIMINARY; PRT; 931 AA.
AC Q7SE30
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU02764.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Quid D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Newes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krysstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Herglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000039; EAA35023.1; -.
DR InterPro: IPR000219; RHOGEF.
DR Pfam: PF00621; RHOGEF; 1.
DR PROSITE; PS00040; DH2; 1.
SQ SEQUENCE 931 AA; 103386 MW; C7F61C7B91B02567 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 931;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 LASSLSA 101
Db 433 LASSLSA 440

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Search completed: October 13, 2005, 18:59:22  
Job time : 231 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2005, 18:47:57 ; Search time 16 Seconds  
(without alignments)  
1310.953 Million cell updates/sec

Title: US-10-694-978-4  
Perfect score: 218  
Sequence: 1 MSFVGENSGVRKMGSEDEKID.....IEFSQPVCVKAEMSPSEVSD 218

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 943

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.7	341	2	T46572
2	8	3.7	413	2	H72606
3	8	3.7	982	2	T06576
4	8	3.7	993	2	T17230
5	8	3.7	1427	2	T39219
6	8	3.7	1622	2	D86428
7	8	3.7	2118	2	T13612
8	7	3.2	116	2	E72509
9	7	3.2	130	2	B72531
10	7	3.2	132	2	F96779
11	7	3.2	133	2	F71189
12	7	3.2	134	2	E64375
13	7	3.2	178	2	JR0264
14	7	3.2	185	2	T49611
15	7	3.2	208	2	T52450
16	7	3.2	240	2	C83702
17	7	3.2	265	2	T42957
18	7	3.2	279	2	B98849
19	7	3.2	290	2	H90001
20	7	3.2	301	2	T18788
21	7	3.2	307	2	F69898
22	7	3.2	356	2	C70025
23	7	3.2	366	2	T26038
24	7	3.2	382	2	F82428
25	7	3.2	421	2	T02135
26	7	3.2	444	2	A11854
27	7	3.2	466	2	E97252
28	7	3.2	506	2	A40679
29	7	3.2	523	2	B40679
					probable UDP-glucose
					hypothetical protein k
					probable protein k
					hypothetical protein
					atp-binding cassette
					glutathione S-conj
					hypothetical protein
					probable non speci
					hypothetical prote
					probable ribosomal
					hypothetical prote
					hypothetical prote
					cyclin I - human
					hypothetical prote
					ribosomal protein
					transcription regu
					hypothetical prote
					prolipoprotein dia
					lipoprotein precu
					hypothetical prote
					hypothetical prote
					multidrug-efflux t
					hypothetical prote
					iron-containing al
					hypothetical prote
					hypothetical prote
					fofi-type Arp synt
					transcription enha
					transcription enha

hypothetical prote  
hypothetical prote  
periplasmic oligop  
hypothetical prote  
uridylyltransferas  
probable membrane  
hypothetical prote  
protein T19E23.7 (neurocan precursor  
neurocan - mouse  
hypothetical prote  
probable potassium  
probable membrane  
tenascin-like prot  
probable guanine n  
cyclic beta 1-2 gl  
protein F14J16.10  
T-cell receptor be  
hypothetical prote  
ferredoxin-NADP re  
hypothetical 9.3K  
ferritin H chain -  
perC protein - Esc  
Clara cell 10K pro  
probable cell surf  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
gene Pax-1 protein  
hypothetical prote  
hypothetical prote  
phage shock protei  
hypothetical 11.6K  
hypothetical 11.6K  
homeotic protein H  
hypothetical prote  
hypothetical prote  
hypothetical prote  
A21L 13.6K protein  
A20L protein - var  
hypothetical prote  
A21L protein - var  
conserved membrane  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
ferritin heavy cha  
hypothetical prote  
probable auxin-ind  
LSU ribosomal prot  
hypothetical prote  
conserved hypothe  
hemoglobin beta ch  
narbonin (clone pN

103	6	2.8	145	2	S76877	hypothetical prote	176	6	2.8	178	1	LGB0
104	6	2.8	146	1	HBTF	hemoglobin beta ch	177	6	2.8	178	2	C71524
105	6	2.8	146	1	HBWA	hemoglobin beta ch	178	6	2.8	180	1	LGST
106	6	2.8	146	1	HBFXB	hemoglobin beta ch	179	6	2.8	180	1	LGSH
107	6	2.8	146	1	HBBP	hemoglobin beta ch	180	6	2.8	180	2	A26986
108	6	2.8	146	1	HBHY	hemoglobin beta ch	181	6	2.8	181	2	S69721
109	6	2.8	146	1	HBMN1	hemoglobin beta ch	182	6	2.8	181	2	A39884
110	6	2.8	146	1	HBOBE	hemoglobin beta ch	183	6	2.8	182	2	S06070
111	6	2.8	146	1	HBTSM	hemoglobin beta ch	184	6	2.8	183	1	FRUHU
112	6	2.8	146	1	HBOVY	hemoglobin beta ch	185	6	2.8	184	2	B90592
113	6	2.8	146	1	HGBAY	hemoglobin gamma c	186	6	2.8	184	2	B72601
114	6	2.8	146	1	HGMQJ	hemoglobin gamma c	187	6	2.8	186	2	F85044
115	6	2.8	146	1	HGMQP	hemoglobin gamma c	188	6	2.8	186	2	S11569
116	6	2.8	146	2	A34947	hemoglobin beta ch	189	6	2.8	186	2	S72228
117	6	2.8	146	2	B29392	hemoglobin beta ch	190	6	2.8	186	2	T09296
118	6	2.8	146	2	B29391	hemoglobin beta ch	191	6	2.8	188	2	AG0273
119	6	2.8	146	2	B25729	hemoglobin beta ch	192	6	2.8	189	2	AG6557
120	6	2.8	146	2	B25359	hemoglobin beta ch	193	6	2.8	190	1	E64705
121	6	2.8	146	2	B24690	hemoglobin beta-S	194	6	2.8	190	2	E71815
122	6	2.8	146	2	JU0163	hemoglobin beta ch	195	6	2.8	192	2	S53555
123	6	2.8	146	2	S11398	PTS fructose-speci	196	6	2.8	197	2	C69877
124	6	2.8	147	1	I37025	hemoglobin gamma-G	197	6	2.8	198	2	T08740
125	6	2.8	147	1	HBM5	hemoglobin beta ma	198	6	2.8	200	2	T01335
126	6	2.8	147	1	HBRT	hemoglobin beta-II	199	6	2.8	201	2	B64685
127	6	2.8	147	1	HGGC	hemoglobin epsilon	200	6	2.8	202	2	T36138
128	6	2.8	147	1	HGGT1	hemoglobin epsilon	201	6	2.8	204	1	S43111
129	6	2.8	147	1	HGMSY2	hemoglobin epsilon	202	6	2.8	206	2	B48441
130	6	2.8	147	1	HGCCZA	hemoglobin gamma-A	203	6	2.8	207	2	F83148
131	6	2.8	147	1	HGCCZG	hemoglobin gamma-G	204	6	2.8	209	2	F84482
132	6	2.8	147	1	HGCC	hemoglobin gamma c	205	6	2.8	209	2	D95274
133	6	2.8	147	1	HGHUA	hemoglobin gamma-A	206	6	2.8	212	1	A1SP2
134	6	2.8	147	1	HGHUG	hemoglobin gamma-G	207	6	2.8	212	2	T01795
135	6	2.8	147	1	HGMQR	hemoglobin gamma-1	208	6	2.8	215	2	C95352
136	6	2.8	147	1	HGMQR2	hemoglobin gamma-2	209	6	2.8	218	2	G86758
137	6	2.8	147	1	I37022	hemoglobin gamma-A	210	6	2.8	220	2	E72210
138	6	2.8	147	2	I77302	hemoglobin gamma c	211	6	2.8	221	2	AG1066
139	6	2.8	147	2	I77303	hemoglobin epsilon	212	6	2.8	221	2	T17997
140	6	2.8	147	2	A42829	hemoglobin epsilon	213	6	2.8	221	2	T10221
141	6	2.8	147	2	A30213	hemoglobin epsilon	214	6	2.8	222	2	A81944
142	6	2.8	147	2	I84437	hemoglobin epsilon	215	6	2.8	224	2	T39158
143	6	2.8	147	2	A49402	hemoglobin epsilon	216	6	2.8	225	2	H75571
144	6	2.8	147	2	I37011	hemoglobin epsilon	217	6	2.8	227	2	B83505
145	6	2.8	147	2	I77304	hemoglobin gamma c	218	6	2.8	228	2	H97336
146	6	2.8	147	2	B42829	hemoglobin gamma c	219	6	2.8	229	1	C71435
147	6	2.8	147	2	I37036	hemoglobin gamma-2	220	6	2.8	229	2	E70978
148	6	2.8	147	2	I37035	hemoglobin gamma-1	221	6	2.8	230	2	S25964
149	6	2.8	147	2	I37002	hemoglobin gamma c	222	6	2.8	231	2	T20959
150	6	2.8	147	2	I37020	hemoglobin gamma-1	223	6	2.8	234	2	T17550
151	6	2.8	147	2	I27800	hemoglobin epsilon	224	6	2.8	234	2	F82440
152	6	2.8	147	2	S00840	hemoglobin beta ch	225	6	2.8	235	2	AG3636
153	6	2.8	147	2	A25747	hemoglobin beta II	226	6	2.8	237	2	AD0084
154	6	2.8	148	2	I77330	hemoglobin gamma c	227	6	2.8	237	2	C83689
155	6	2.8	150	1	NEEB1C	gene 57B protein -	228	6	2.8	241	2	H86135
156	6	2.8	152	1	ZBBPT4	anthranilate synth	229	6	2.8	241	2	S56592
157	6	2.8	153	2	H86034	hypothetical prote	230	6	2.8	241	2	B71128
158	6	2.8	153	2	G91187	hypothetical prote	231	6	2.8	241	2	B71128
159	6	2.8	153	2	S47817	hypothetical 18.1K	232	6	2.8	242	2	D81161
160	6	2.8	154	2	F86306	F20D23.22 protein	233	6	2.8	242	2	T48581
161	6	2.8	155	4	S21403	hemoglobin gamma-G	234	6	2.8	246	2	F84412
162	6	2.8	161	1	D69256	hypothetical prote	235	6	2.8	246	2	AB0261
163	6	2.8	158	1	H82210	probable acetyltra	236	6	2.8	248	2	A29624
164	6	2.8	162	1	LGUIT	beta-lactoglobulin	237	6	2.8	248	2	AH3575
165	6	2.8	162	2	S00132	beta-lactoglobulin	238	6	2.8	250	2	F95218
166	6	2.8	164	2	I46710	ferritin heavy cha	239	6	2.8	250	2	D98082
167	6	2.8	164	2	T16168	hypothetical prote	240	6	2.8	251	2	B64337
168	6	2.8	166	2	T48040	hypothetical prote	241	6	2.8	252	2	H83390
169	6	2.8	168	2	F72481	hypothetical prote	242	6	2.8	252	2	D88338
170	6	2.8	169	2	C75427	hypothetical prote	243	6	2.8	253	2	E72302
171	6	2.8	169	2	B75490	hypothetical prote	244	6	2.8	253	2	T17312
172	6	2.8	170	2	B71548	hypothetical prote	245	6	2.8	253	2	G81389
173	6	2.8	173	2	G87383	hypothetical prote	246	6	2.8	254	2	E97358
174	6	2.8	173	2	C84684	acetyltransferase,	247	6	2.8	254	2	E75052
175	6	2.8	174	2	A41358	hypothetical prote	248	6	2.8	256	2	C96937
						gag polyprotein -	249	6	2.8			

249	6	2.8	259	1	B64251	probable methyltra	322	6	2.8	300	2	S73528	probable lipoprote
250	6	2.8	259	2	F70032	ABC transporter (A	323	6	2.8	300	2	T29112	hypothetical prote
251	6	2.8	261	2	S63604	homeobox protein G	324	6	2.8	302	2	F75619	probable hemin ABC
252	6	2.8	262	1	A31372	granzyme A (EC 3.4	325	6	2.8	303	2	E81348	binding-protein de
253	6	2.8	264	2	H71804	ribosomal protein	326	6	2.8	304	2	S59414	hypothetical prote
254	6	2.8	264	2	B64714	probable ABC trans	327	6	2.8	305	2	C85042	SRA1-like syntaxin
255	6	2.8	264	2	E95410	glucosamine-6-phos	328	6	2.8	305	2	A75211	asparaginase (EC 3
256	6	2.8	266	2	H82387	dinucleotide-utili	329	6	2.8	305	2	T24534	hypothetical prote
257	6	2.8	266	2	F97259	conserved hypotcet	330	6	2.8	305	2	A71247	probable L-asparag
258	6	2.8	266	2	F90056	3'-phosphoadenosin	331	6	2.8	306	2	A72668	probable spermidin
259	6	2.8	267	2	H83426	DNA-formamidopyrim	332	6	2.8	306	2	A86407	unknown protein li
260	6	2.8	269	1	DBCECP	formamidopyrimidin	333	6	2.8	307	2	C97404	hypothetical prote
261	6	2.8	269	2	AG0971	formamidopyrimidin	334	6	2.8	307	2	S62472	probable Methylthi
262	6	2.8	269	2	G86039	formamidopyrimidin	335	6	2.8	307	2	B38448	acylttransferase (E
263	6	2.8	269	2	F91192	formamidopyrimidin	336	6	2.8	307	2	S11686	transcription regu
264	6	2.8	270	2	F64050	glucosamine-6-phos	337	6	2.8	307	2	F87389	hypothetical prote
265	6	2.8	270	2	T43039	hypothetical prote	338	6	2.8	309	2	B84550	hypothetical prote
266	6	2.8	271	2	G87071	hypothetical prote	339	6	2.8	310	2	T39024	probable eukaryoti
267	6	2.8	271	2	T18056	ATPase homolog A55	340	6	2.8	311	2	T38934	hypothetical prote
268	6	2.8	271	2	B86918	hypothetical prote	341	6	2.8	311	2	G86336	hypothetical prote
269	6	2.8	271	2	S12560	transcription fact	342	6	2.8	314	2	T15045	spermidine synthas
270	6	2.8	272	2	G71115	hypothetical prote	343	6	2.8	314	2	S52223	hypothetical prote
271	6	2.8	273	1	E64625	hydroxyethylthiaz	344	6	2.8	314	2	T03524	cobD protein - Rho
272	6	2.8	273	2	AC0294	Conserved hypotcet	345	6	2.8	314	2	A36195	developmental prot
273	6	2.8	274	2	G70653	probable glpQ1 pro	346	6	2.8	314	2	A41544	developmental prot
274	6	2.8	275	2	F71714	2-dehydro-3-deoxyp	347	6	2.8	315	1	K1EBRT	ribose-phosphate d
275	6	2.8	276	2	S56696	narbonin (clone pN	348	6	2.8	315	1	K1ECRY	ribose-phosphate d
276	6	2.8	276	2	S74745	ABC-type transport	349	6	2.8	315	2	E85700	phosphoribosylpyro
277	6	2.8	277	1	Q0ECAD	probable membrane	350	6	2.8	315	2	AF0720	ribose-phosphate d
278	6	2.8	277	2	I47162	Ig gamma 4 chain c	351	6	2.8	315	2	H90842	phosphoribosylpyro
279	6	2.8	277	2	AC0704	conserved hypotcet	352	6	2.8	315	2	AG0245	ribose-phosphate d
280	6	2.8	277	2	F85778	hypothetical prote	353	6	2.8	315	2	E83369	probable transcrip
281	6	2.8	277	2	B90930	hypothetical prote	354	6	2.8	315	2	T42682	hypothetical prote
282	6	2.8	277	2	D82392	conserved hypotcet	355	6	2.8	317	2	G82635	methanol dehydroge
283	6	2.8	279	2	S73526	probable lipoprote	356	6	2.8	320	2	G88989	protein C36C5.8 li
284	6	2.8	279	2	S75552	hypothetical prote	357	6	2.8	321	2	A84792	hypothetical prote
285	6	2.8	279	2	H87917	protein F28D9.1 [i	358	6	2.8	322	2	C82293	riboflavin kinase/
286	6	2.8	279	2	B72481	hypothetical prote	359	6	2.8	325	2	T25331	hypothetical prote
287	6	2.8	280	2	S47815	hypothetical 31.8K	360	6	2.8	325	2	S65306	hypothetical prote
288	6	2.8	280	2	F86034	hypothetical prote	361	6	2.8	326	2	S28706	hypothetical prote
289	6	2.8	280	2	H75151	abc transporter, A	362	6	2.8	327	2	B75341	probable oxidoredu
290	6	2.8	281	2	S08410	probable transcrip	363	6	2.8	328	2	I47160	Ig gamma 2b chain
291	6	2.8	281	2	S18541	hypothetical prote	364	6	2.8	328	2	I47161	Ig gamma 3 chain c
292	6	2.8	283	2	T31122	probable transcrip	365	6	2.8	328	2	I47158	Ig gamma 1 chain c
293	6	2.8	283	2	S73534	probable lipoprote	366	6	2.8	328	2	I47159	Ig gamma 2a chain
294	6	2.8	283	2	S73523	probable lipoprote	367	6	2.8	329	2	D72669	hypothetical prote
295	6	2.8	284	2	AC2622	hypothetical prote	368	6	2.8	329	2	S63135	hypothetical prote
296	6	2.8	284	2	B1343	transcription regu	369	6	2.8	329	2	T65768	smooth muscle myos
297	6	2.8	284	2	D81075	conserved hypotcet	370	6	2.8	330	2	A75480	lipoic acid syntha
298	6	2.8	284	2	D81866	hypothetical prote	371	6	2.8	331	2	F85873	cell division prot
299	6	2.8	284	2	AF2491	hypothetical prote	372	6	2.8	331	2	E91029	cell division prot
300	6	2.8	284	2	AF1713	transcription regu	373	6	2.8	331	2	G65004	Div protein - Esch
301	6	2.8	284	2	G71132	probable cobalt tr	374	6	2.8	331	2	A75323	probable chromosom
302	6	2.8	285	2	S49880	hypothetical narbo	375	6	2.8	331	2	H90576	lipoprotein d limp
303	6	2.8	285	2	T51576	hypothetical prote	376	6	2.8	332	2	WZBYR	arginase (EC 3.5.3
304	6	2.8	289	1	S72862	cysQ homolog - Myc	377	6	2.8	333	1	T37871	hypothetical nucle
305	6	2.8	289	2	A83656	hypothetical prote	378	6	2.8	333	2	T36449	hypothetical prote
306	6	2.8	290	2	F90332	hypothetical prote	379	6	2.8	333	2	RDECEP	N-acetyl-gamma-glu
307	6	2.8	290	2	A93371	hypothetical prote	380	6	2.8	334	1	RDECEP	hypothetical prote
308	6	2.8	290	2	T09363	hypothetical prote	381	6	2.8	334	1	KHRTL	cathepsin L (EC 3.
309	6	2.8	291	2	S56697	narbonin (clone pN	382	6	2.8	334	1	KHRTL	cathepsin L (EC 3.
310	6	2.8	291	2	S56698	narbonin (clone pN	383	6	2.8	334	2	AB0936	N-acetyl-gamma-glu
311	6	2.8	292	2	T49261	hypothetical prote	384	6	2.8	334	2	G91239	N-acetyl-gamma-glu
312	6	2.8	293	2	B90159	porphobilinogen de	385	6	2.8	334	2	D86087	N-acetyl-gamma-glu
313	6	2.8	295	2	T51350	RNA helicase RH31	386	6	2.8	334	2	F86372	Spermidine synthas
314	6	2.8	295	4	S36174	RNA binding protei	387	6	2.8	334	2	A39605	transcription regu
315	6	2.8	296	2	I52860	smooth muscle myos	388	6	2.8	334	2	T21503	hypothetical prote
316	6	2.8	296	2	AD0467	probable membrane	389	6	2.8	336	2	E75040	hydrogenase expres
317	6	2.8	296	2	H83480	cytochrome o ubiqu	390	6	2.8	336	2	D71121	probable hydrogena
318	6	2.8	296	2	G97799	hypothetical prote	391	6	2.8	336	2	G95003	membrane protein (
319	6	2.8	298	2	T09975	H <sub>2</sub> -transporting tw	392	6	2.8	337	1	WMBE32	ribonucleoside-dip
320	6	2.8	298	2	F90495	conserved hypotcet	393	6	2.8	337	1	WMBE32	ribonucleoside-dip
321	6	2.8	300	2	G95954	probable dTDP-4-de	394	6	2.8	337	2	C36953	acetoin[2,6-dichlo



395	6	2.8	339	2	E89878	hypotheical prote	468	6	2.8	408	2	T02133	hypotheical prote
396	6	2.8	340	2	T01492	spermidine synthas	469	6	2.8	409	2	C82036	multidrug resistan
397	6	2.8	341	2	F75193	asparaginase (bc 3	470	6	2.8	410	2	S44626	C503.8 protein -
398	6	2.8	340	2	B97876	conserved hypothe	471	6	2.8	410	2	D98177	hypotheical prote
399	6	2.8	341	2	T31826	hypotheical prote	472	6	2.8	411	2	C64052	NADH2 dehydrogen
400	6	2.8	341	2	S40612	myosin-related pro	473	6	2.8	412	2	H87281	thiolase family pr
401	6	2.8	341	2	AG2880	ABC transporter, s	474	6	2.8	412	2	S07537	myosin heavy chain
402	6	2.8	341	2	G97856	conserved hypothe	475	6	2.8	413	2	S61305	cych protein - Par
403	6	2.8	342	2	T22742	hypotheical prote	476	6	2.8	413	2	AI0598	probable phospholi
404	6	2.8	343	2	AG1273	N-acetylglutamate	477	6	2.8	413	2	AF1427	an hypotheical pr
405	6	2.8	343	2	T08442	hypotheical prote	478	6	2.8	414	2	AI2544	hypotheical prote
406	6	2.8	344	2	A72780	probable ribosomal	479	6	2.8	415	2	A35560	lysosomal membrane
407	6	2.8	345	2	AG3186	hypotheical prote	480	6	2.8	416	2	G84108	cell wall lytic ac
408	6	2.8	345	2	S51548	killer toxin K28 -	481	6	2.8	417	2	B71034	hypotheical prote
409	6	2.8	345	2	AE2914	conserved hypothe	482	6	2.8	418	2	AE2965	exopolysaccharide
410	6	2.8	345	2	H97688	hypotheical prote	483	6	2.8	418	2	H98317	MITF protein - hum
411	6	2.8	346	2	S56665	trypophan synthas	484	6	2.8	419	2	I38024	microphthalma-ass
412	6	2.8	347	2	D84333	alcohol dehydrogen	485	6	2.8	419	2	A40728	hypotheical prote
413	6	2.8	348	2	A57234	lin-44 protein pre	486	6	2.8	419	2	C40901	hypotheical prote
414	6	2.8	348	2	S57601	ribonuclease H (EC	487	6	2.8	420	2	B97843	glycine hydroxymet
415	6	2.8	348	2	T29515	hypotheical prote	488	6	2.8	421	2	B82062	conserved hypothe
416	6	2.8	349	2	S74439	iron(III) diclitrat	489	6	2.8	425	1	F0MVG	gag polyprotein -
417	6	2.8	349	2	B99420	hypotheical prote	490	6	2.8	426	2	T06086	probable protein s
418	6	2.8	351	2	T40854	hypotheical prote	491	6	2.8	426	2	C75297	hypotheical prote
419	6	2.8	352	2	T04841	protein kinase hom	492	6	2.8	427	1	C64408	hypotheical prote
420	6	2.8	352	2	T25170	hypotheical prote	493	6	2.8	429	1	F0LJCN	gag polyprotein -
421	6	2.8	356	2	T19015	hypotheical prote	494	6	2.8	429	1	F0LJGH	probable gag poly
422	6	2.8	356	2	AH1881	hypotheical prote	495	6	2.8	429	2	S06073	gag polyprotein -
423	6	2.8	357	2	A95888	probable ABC trans	496	6	2.8	429	2	T22495	hypotheical prote
424	6	2.8	360	2	F69342	DNA primase homol	497	6	2.8	431	2	H82237	histidinol dehydro
425	6	2.8	361	2	A40023	paired box homolog	498	6	2.8	431	2	T46187	polygalacturonase
426	6	2.8	364	2	T35353	hypotheical prote	499	6	2.8	432	2	T23762	hypotheical prote
427	6	2.8	365	2	T28184	hypotheical prote	500	6	2.8	434	2	G95124	Grp-binding protei
428	6	2.8	367	2	A83681	ABC transporter (p	501	6	2.8	435	2	T15737	hypotheical prote
429	6	2.8	369	2	H82357	tRNA (uracil-5-)-m	502	6	2.8	435	2	T19687	hypotheical prote
430	6	2.8	370	1	B43673	chloromuconate cyc	503	6	2.8	436	2	A37953	transcription regu
431	6	2.8	370	2	AH2161	cobalamn biosynth	504	6	2.8	436	2	H97594	Grp-binding protei
432	6	2.8	370	2	S75625	hypotheical prote	505	6	2.8	436	2	G71862	alpha-(1,3)-fucosy
433	6	2.8	370	2	T32615	hypotheical prote	506	6	2.8	437	2	F70114	probable zinc prot
434	6	2.8	371	2	F83487	hypotheical prote	507	6	2.8	437	2	B53193	hedgheg homolog v
435	6	2.8	371	2	B84709	hypotheical prote	508	6	2.8	441	2	JC7653	pectate lyase (EC
436	6	2.8	372	2	T17474	chalcone synthase	509	6	2.8	441	2	E72579	hypotheical prote
437	6	2.8	372	2	T23680	hypotheical prote	510	6	2.8	441	2	C95307	probable transport
438	6	2.8	372	2	T49008	melanocortin-5, rec	511	6	2.8	442	2	F71930	probable transport
439	6	2.8	373	2	D71428	cysteine proteinas	512	6	2.8	442	2	A64582	sodium- and chlori
440	6	2.8	377	2	C89300	protein RliG11.9 [	513	6	2.8	444	2	E69102	sensory transducti
441	6	2.8	378	2	T19012	hypotheical prote	514	6	2.8	445	2	A56024	GDP dissociation i
442	6	2.8	380	2	C84710	hypotheical prote	515	6	2.8	445	2	C56956	rab GDP dissociati
443	6	2.8	382	2	D70587	probable dnaJ2 pro	516	6	2.8	445	2	B54091	protein F20N2.10 [
444	6	2.8	382	2	T49724	hypotheical prote	517	6	2.8	445	2	A96599	hypotheical prote
445	6	2.8	385	2	E83414	conserved hypothe	518	6	2.8	446	2	D71418	amino acid transpo
446	6	2.8	387	2	B75211	multidrug resistan	519	6	2.8	446	2	H90507	hypotheical prote
447	6	2.8	387	2	H72862	hypotheical prote	520	6	2.8	446	2	S28086	gene A protein - y
448	6	2.8	387	2	T41844	AcMPV orf103 - Bo	521	6	2.8	447	2	C82958	probable two-compo
449	6	2.8	387	2	B71247	hypotheical prote	522	6	2.8	447	2	C82958	glycerol dehydroge
450	6	2.8	389	2	T38455	hypotheical prote	523	6	2.8	450	2	T37628	glucoamylase precu
451	6	2.8	389	2	E95422	probable transmemb	524	6	2.8	450	2	T39433	flagellar hook-len
452	6	2.8	390	2	AH0260	conserved hypothe	525	6	2.8	450	2	AG0222	tailless (tll) pro
453	6	2.8	390	2	F81393	probable altronate	526	6	2.8	452	2	B47265	tailless (tll) pro
454	6	2.8	392	2	H71520	probable hch trans	527	6	2.8	452	2	A35602	tailless (tll) pro
455	6	2.8	392	2	F81676	heat shock gene re	528	6	2.8	453	2	A96688	hypotheical prote
456	6	2.8	393	2	AH3109	MPS permease [suga	529	6	2.8	454	1	TVRTAR	thyroid hormone re
457	6	2.8	396	2	F69813	multidrug-efflux t	530	6	2.8	454	2	B71914	alpha (1,3)-fucosy
458	6	2.8	397	2	T36119	hypotheical prote	531	6	2.8	454	2	D85020	hypotheical prote
459	6	2.8	397	2	AD3403	general L-amino ac	532	6	2.8	455	2	AB0909	serine protease (E
460	6	2.8	398	2	B70752	hypotheical prote	533	6	2.8	455	2	C91142	serine endoprotein
461	6	2.8	400	2	T05629	hypotheical prote	534	6	2.8	455	2	F85987	serine endoprotein
462	6	2.8	404	2	H87106	probable integral	535	6	2.8	455	2	JC6051	trypsin-like prote
463	6	2.8	404	2	AG2174	hypotheical prote	536	6	2.8	455	2	H84955	UDP-N-acetylmuramo
464	6	2.8	407	2	AB2904	argininosuccinate	537	6	2.8	455	2	F83460	probable amino aci
465	6	2.8	407	2	A11159	flagellar biosynth	538	6	2.8	457	2	D90067	hypotheical prote
466	6	2.8	407	2	A11518	flagellar biosynth	539	6	2.8	457	2	AF2975	aminotransferase,
467	6	2.8	408	2	H87264	argininosuccinate	540	6	2.8	457	2	E98307	probable aminotran

541	6	2.8	458	2	AD2437	hypothetical prote	614	514	2	T42402	importin alpha 1 -
542	6	2.8	459	2	A39932	hypothetical prote	615	515	2	A69759	1-pyrroline-5-carb
543	6	2.8	460	2	D97679	argininosuccinate	616	516	2	F88618	protein W06F12.2 [
544	6	2.8	461	2	S69046	hypothetical prote	617	517	1	D37831	phenol 2-monooxyge
545	6	2.8	462	2	T30073	hypothetical prote	618	517	2	T10927	3C3.18c protein
546	6	2.8	461	2	A72779	hypothetical prote	619	520	2	G87343	cytochrome d ubiqu
547	6	2.8	463	1	P2ML13	L2 protein - human	620	520	2	C70776	probable export pr
548	6	2.8	465	2	S74905	hypothetical prote	621	520	2	T14752	microphthalmia-ass
549	6	2.8	465	2	A30306	probable amino aci	622	522	2	T36501	probable serine/th
550	6	2.8	467	2	T04540	adenylosuccinate 1	623	522	2	T24144	hypothetical prote
551	6	2.8	468	2	B69967	Na+/H+-exchanging	624	523	2	S42727	translation initia
552	6	2.8	470	2	T22785	hypothetical prote	625	524	1	S76810	probable NAHD2 deh
553	6	2.8	472	1	YX0UM	citrate (tsi)-synth	626	524	2	S44982	flagellin - Shigel
554	6	2.8	472	2	H97238	pyridine transhydr	627	525	2	G83173	GMP synthase PA376
555	6	2.8	473	2	I50420	nonerythroid alpha	628	526	2	T07082	lycopene epsilon-c
556	6	2.8	473	2	G84312	glycine dehydrogen	629	530	2	S62439	hypothetical serin
557	6	2.8	475	2	B27671	spectrin alpha cha	630	531	2	E64106	2-isopropylmalate
558	6	2.8	475	2	A27671	spectrin alpha cha	631	532	2	T38326	serine threonine p
559	6	2.8	476	2	C64601	fucosyltransferase	632	532	2	A57173	oculocutaneous alb
560	6	2.8	476	2	T40330	hypothetical prote	633	533	2	AD0726	conserved hypothet
561	6	2.8	478	2	G90514	nadh oxidase (nox)	634	533	2	JS0304	developmental cont
562	6	2.8	481	2	H71084	hypothetical prote	635	535	2	T41384	hypothetical prote
563	6	2.8	483	2	D87290	conserved hypothet	636	536	1	F0MVMD	gag polyprotein -
564	6	2.8	484	2	B33501	myosin heavy chain	637	537	2	H64241	arginine-trNA liga
565	6	2.8	487	2	F82065	RNA polymerase sig	638	539	2	G69875	hypothetical prote
566	6	2.8	487	2	AD0818	probable exported	639	540	2	E71503	probable adp/atp t
567	6	2.8	487	2	H83104	hypothetical prote	640	541	2	T48811	hypothetical prote
568	6	2.8	488	2	A55180	homeotic protein H	641	544	2	A55146	guanine nucleotide
569	6	2.8	489	2	T03949	serine-trNA ligase	642	546	2	T37516	major facilitator
570	6	2.8	489	2	S09637	flagellin - Salmon	643	547	1	S52489	choline oxidase (E
571	6	2.8	489	2	S69027	ammonium transport	644	547	2	AH0098	TCP-1 containing c
572	6	2.8	492	2	S06907	thyroid hormone re	645	548	2	JC4073	probable methyl-ac
573	6	2.8	492	2	I57696	c-erba-alpha-2-rel	646	548	2	T05738	probable transcrip
574	6	2.8	492	2	D71510	probable oligopept	647	550	2	B97346	oligopeptide ABC t
575	6	2.8	492	2	G81668	peptide ABC transp	648	550	2	H86516	fructose-6-P phosp
576	6	2.8	494	2	A82294	probable carbon st	649	550	2	A72106	pyrophosphate-fruc
577	6	2.8	495	2	C89778	hypothetical prote	650	552	2	T24812	hypothetical prote
578	6	2.8	497	2	S43745	phosphatidylinosit	651	552	2	T23755	hypothetical prote
579	6	2.8	500	1	F75342	IMP dehydrogenase	652	556	2	S51892	probable membrane
580	6	2.8	500	2	T06332	dihydrolipoamide d	653	557	2	T16696	hypothetical prote
581	6	2.8	501	2	T45856	hypothetical prote	654	559	2	T43071	activation/secreti
582	6	2.8	502	2	A98151	dipeptide transpor	655	560	2	S38035	probable serine/th
583	6	2.8	502	2	AC3137	hypothetical prote	656	560	2	T16589	hypothetical prote
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585	6	2.8	504	2	S33190	phase-1 flagellin	658	562	2	T26242	hypothetical prote
586	6	2.8	504	2	S33188	phase-1 flagellin	659	562	2	T51348	RNA helicase RH25
587	6	2.8	504	2	S33187	phase-1 flagellin	660	568	2	T26243	hypothetical prote
588	6	2.8	504	2	S33191	phase-1 flagellin	661	569	2	S57812	leucyl aminopeptid
589	6	2.8	504	2	S33194	phase-1 flagellin	662	578	2	S74578	probable flavoprot
590	6	2.8	504	2	S33186	phase-1 flagellin	663	580	2	T43485	hypothetical prote
591	6	2.8	504	2	S33189	phase-1 flagellin	664	592	2	E70455	sulfur oxidation p
592	6	2.8	504	2	A33286	acetyl-CoA C-acety	665	592	2	A96523	hypothetical prote
593	6	2.8	505	1	S38534	cytochrome P450 76	666	592	2	H97105	carbon starvation
594	6	2.8	507	2	E64247	phosphoglycerate m	667	593	2	H64594	multidrug resistan
595	6	2.8	507	2	S33185	phase-1 flagellin	668	595	2	T51747	DNA helicase RH26
596	6	2.8	507	2	S33192	phase-1 flagellin	669	602	2	AF3490	DNA-directed RNA p
597	6	2.8	507	2	T50398	hypothetical serin	670	602	2	H87503	phosphogluconate d
598	6	2.8	507	2	F36033	probable sugar upt	671	606	2	B95950	probable two-compo
599	6	2.8	507	2	D98330	hypothetical prote	672	608	2	AD2590	two component sens
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601	6	2.8	508	1	O4CHC7	steroid 17alpha-mo	674	610	2	AG0227	exonuclease ABC c
602	6	2.8	508	2	A53465	phase 1 flagellin	675	610	2	PN0012	mucin 4, tracheal
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605	6	2.8	508	2	C95282	probable ABC trans	678	615	2	D64714	cell division prot
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607	6	2.8	510	2	T45952	hypothetical prote	680	621	2	S10450	myosin heavy chain
608	6	2.8	511	2	T31899	hypothetical prote	681	623	2	T47874	scarecrow-like pro
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610	6	2.8	512	1	A55407	IMP dehydrogenase	683	625	2	G90570	hypothetical prote
611	6	2.8	513	2	A05029	proteochlorophyllid	684	627	2	H82573	exonuclease ABC s
612	6	2.8	513	2	G81298	probable periplasm	685	627	2	T26064	hypothetical prote
613	6	2.8	514	1	A38668	IMP dehydrogenase	686	631	2	B42603	beta-glucoside-spe

687 JC5896 2 2.8 635 6 killer cell inhibi  
688 A54000 2 2.8 637 6 sodium/phosphate c  
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702 D96549 2 2.8 651 6 protein hypothetic  
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718 C83052 2 2.8 667 6 protein F8K7.9 lim  
719 H86349 2 2.8 668 6 hypothetrical prote  
720 S40710 2 2.8 669 6 hypothetrical prote  
721 T22127 2 2.8 670 6 antibiotic transpo  
722 C40046 2 2.8 671 6 NF-AT component -  
723 S45262 2 2.8 672 6 guanosine-3',5'-bi  
724 B81058 2 2.8 673 6 hypothetrical prote  
725 T29708 2 2.8 674 6 transcription fact  
726 JC5805 2 2.8 675 6 gluconate transpor  
727 T43327 2 2.8 676 6 VPS45-like protein  
728 D71607 2 2.8 677 6 guanosine-3',5'-bi  
729 B81819 2 2.8 678 6 probable secretion  
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742 S34683 2 2.8 691 6 yTA6 protein - yea  
743 S61113 2 2.8 692 6 female sterile hom  
744 A56619 2 2.8 693 6 hypothetrical prote  
745 T20109 2 2.8 694 6 FixI protein - Rhi  
746 C32052 2 2.8 695 6 FixII copper trans  
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751 JC5112 2 2.8 700 6 UBF transcription  
752 A40439 2 2.8 701 6 regulatory protein  
753 S70962 2 2.8 702 6 transcription fact  
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756 D91195 2 2.8 705 6 hypothetrical prote  
757 B86042 2 2.8 706 6 hypothetrical 88.1  
758 B65167 2 2.8 707 6 carnitine palmitoy  
759 A46627 2 2.8 708 6

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H56611 2  
JC5799 2  
T30853 2  
E86165 2

ATP-dependent prot  
malate dehydrogena  
neuroendocrine-spe  
hypothetrical prote  
probable 60kda inn  
hypothetrical prote  
1-phosphatidylinos  
hypothetrical prote  
phenylalanine-tRNA  
titin, muscle - ch  
hypothetrical prote  
glycerol-3-phospha  
gene coxII intron  
probable outer mem  
condensin complex  
protein kinase hom  
argonaute-like pro  
probable protein p  
gene DN10 protein  
yeless, long form  
RNA replicase 2a -  
killer cell inhibi  
pullulanase - Ther  
hypothetrical prote  
retrovirus-related  
clpB protein VC071  
probable membrane  
hypothetrical prote  
conserved hypotet  
probable capsid-as  
probable replicati  
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puff 74E protein -  
alanyl-CRNA synthe  
DNA mismatch repai  
ubiquitin-protein  
miss protein limpo  
hypothetrical prote  
SIN1-associated pr  
alanyl-CRNA synthe  
hypothetrical prote  
probable regulator  
surface-layer prot  
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probable exincule  
probable serine/th  
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endopeptidase clp  
hypothetrical prote  
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polyketide synthas  
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hypothetrical prote  
probable adhesin 2  
alpha-D-mannosidas  
antigenic heat-sta  
FltK9.2 protein -

833 6 2.8 1026 2 C97783 cell surface antigen  
834 6 2.8 1030 2 A32612 spectrin alpha chain  
835 6 2.8 1035 1 GNFPG1 HIV-1 retropepsin  
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837 6 2.8 1051 2 A38373 ubiquitin-protein  
838 6 2.8 1061 2 S75508 acriflavin resista  
839 6 2.8 1063 2 D86731 hypothetical prote  
840 6 2.8 1075 2 T45570 kinesin-like prote  
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846 6 2.8 1123 2 A39962 kinase-related tra  
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858 6 2.8 1212 2 T42387 histocompatibility  
859 6 2.8 1214 2 JC2069 zinc-finger protei  
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894 6 2.8 1615 2 T06510 ABC transporter At  
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899 6 2.8 1734 2 A54602 hypothetical prote  
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915 6 2.8 2321 2 S78549 notch3 protein - h  
916 6 2.8 2401 2 T28676 rhoptry protein - h  
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919 6 2.8 2477 1 SJCHA spectrin alpha cha  
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928 6 2.8 2843 1 RBHUAP adenomatous polypo  
929 6 2.8 2845 2 I49505 adenomatous polypo  
930 6 2.8 3005 2 T08841 polyprotein - dour  
931 6 2.8 3010 1 GNVVTV genome polyprotein  
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933 6 2.8 3169 2 T00296 toxin B - Escheric  
934 6 2.8 3187 2 JC5837 364K Golgi complex  
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937 6 2.8 3828 2 T13857 trithorax protein  
938 6 2.8 4077 2 T17484 hypothetical prote  
939 6 2.8 4351 2 T00252 MEGF1 protein - ra  
940 6 2.8 4377 2 A55575 ankryrin 3, long sp  
941 6 2.8 5627 2 C83339 hypothetical prote  
942 6 2.8 10223 2 T30225 polyketide synthas  
943 6 2.8 26926 1 I38344 titin, cardiac mus

## ALIGNMENTS

## RESULT 1

T46572  
probable UDP-glucuronic acid epimerase (EC 5.1.3.-) [imported] - Sinorhizobium meliloti  
C:Species: Sinorhizobium meliloti  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46572  
R:Kereszt, A.; Kiss, E.; Reuhs, B.L.; Carlson, R.W.; Kondoros, A.; Putnok, P.  
J. Bacteriol. 180, 5426-5431, 1998  
A:Title: Novel rkp gene clusters of Sinorhizobium meliloti involved in capsular polysac  
A:Reference number: 223086; MUID:98440435; PMID:9765575  
A:Accession: T46572  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-341 <KER>  
A:Cross-references: UNIPROT:O54067; EMBL:AJ222661; NID:g2959982; PIDN:CAA10917.1; PID:g2  
A:Experimental source: strain 41  
C:Genetics:  
A:Note: lpsL  
C:Function:  
A:Description: required for the synthesis of rhizobial capsular polysaccharide [validate  
C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology  
C:Keywords: isomerase

Query Match 3.7%; Score 8; DB 2; Length 341;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 161 VGSWNMLE 168

Db 105 VGSWNMLE 112

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RESULT 2
H72606
hypothetical protein APE1319 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72606
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6. 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 <KAW>
A;Cross-references: UNIPROT:Q9YCD8; DDBJ:AP000061; NID:g5104821; PIDN:BAAR80310.1; PID:d1
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1319

Query Match 3.7%; Score 8; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 LASSLSA 101
Db 12 LASSLSA 19

RESULT 3
T06576
probable protein kinase TCCR2 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06576
R;Hackett, R.W.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z15770
A;Accession: T06576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-982 <HAC>
A;Cross-references: UNIPROT:O65833; EMBL:AJ005077; NID:e1296722; PIDN:CAA06334.1; PID:e1
A;Experimental source: cultivar Ailsa craig
C;Genetics:
A;Gene: TCCR2

Query Match 3.7%; Score 8; DB 2; Length 982;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 ASSLSAS 102
Db 30 ASSLSAS 37

RESULT 4
T17230
hypothetical protein DKFPz434E066.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17230
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18722
A;Accession: T17230
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-993 <KOE>
A;Cross-references: UNIPROT:Q9UES6; EMBL:AL117432
A;Experimental source: adult testis; clone DKFPz434E066
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C;Genetics:  
A;Note: DKFPz434E066.1

Query Match 3.7%; Score 8; DB 2; Length 993;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
Db 7 ALASSLS 14

## RESULT 5

T39219  
atp-binding cassette transporter abc1 - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T39219  
R;McDougall, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21836  
A;Accession: T39219  
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA  
A;Residues: 1-1427 <MCD>  
A;Cross-references: UNIPROT:Q92337; EMBL:Z99262; PIDN:CAB16410.1; GSPDB:GN00066; SPDB:SPJ  
A;Experimental source: strain 972h-; cosmid c9E9  
C;Genetics:  
A;Gene: SPDB:SPAC9E9.12c  
A;Map position: 1  
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1427;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLD 75  
Db 1391 KVLVLD 1398

## RESULT 6

D86428  
glutathione S-conjugate transporting ATPase (AtMRP1) - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: D86428

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86428  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1622 <STO>  
A;Cross-references: UNIPROT:Q9C8G9; GB:AE005172; NID:g11055814; PIDN:AAG28284.1; GSPDB:GN  
C;Genetics:

A;Map position: 1  
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1622;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLD 75

Db 1440 KVLVDSG 1447

## RESULT 7

T13612

hypothetical protein 8D8.1 - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C:Accession: T13612

R:Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A:Reference number: Z17695

A:Accession: T13612

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2118 <PAP>

A:Cross-references: UNIPROT:O76904; EMBL:AL022018; PIDN:CAAL17682.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0024367

A:Introns: 47/3; 726/3; 770/1; 813/3; 1404/1; 1473/3

A>Note: EG:8D8.1

C:Superfamily: *Drosophila* hypothetical protein EG\_8D8.1

## Query Match

Best Local Similarity 3.7%; Score 8; DB 2; Length 2118;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SSSLSSASA 103

|||||

Db 76 SSSLSSASA 83

## RESULT 8

E72509

probable non specific lipid-transfer protein APE2051 - *Aeropyrum pernix* (strain K1)

C:Species: *Aeropyrum pernix*

C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: E72509

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic *Crenarchaeon*, *Aeropyr*

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: E72509

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-116 <KAW>

A:Cross-references: UNIPROT:Q9YA88; DDBJ:AP000063; NID:G5105654; PIDN:BAA81061.1; PID:dl

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2051

## Query Match

Best Local Similarity 3.2%; Score 7; DB 2; Length 116;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SSSLSSAS 102

|||||

Db 39 SSSLSSAS 45

## RESULT 9

B72531

hypothetical protein APE2222 - *Aeropyrum pernix* (strain K1)

C:Species: *Aeropyrum pernix*

C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: B72531

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic *Crenarchaeon*, *Aeropyr*

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: B72531

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <KAW>

A:Cross-references: UNIPROT:Q9Y9R6; DDBJ:AP000063; NID:G5105654; PIDN:BAA81234.1; PID:dl

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2222

## Query Match

Best Local Similarity 3.2%; Score 7; DB 2; Length 130;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 LSSASAE 104

|||||

Db 45 LSSASAE 51

## RESULT 10

F96779

probable ribosomal protein S9 F9E10.17 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: F96779

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96779

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <STO>

A:Cross-references: UNIPROT:Q9C9P6; GB:AE005173; NID:G6646766; PIDN:AAF21078.1; GSPDB:GN

C:Genetics:

A:Gene: F9E10.17

A:Map position: 1

C:Superfamily: ribosomal protein S9/S16

## Query Match

Best Local Similarity 3.2%; Score 7; DB 2; Length 132;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 LASSLSS 100

|||||

Db 7 LASSLSS 13

## RESULT 11

F71189

hypothetical protein PH1790 - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004

C:Accession: F71189

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: F71189

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-133 <KAW>

A:Cross-references: UNIPROT:O59454; GB:AP000007; NID:G3236134; PIDN:BAA30909.1; PID:G325

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A;Gene: PH1790

```
Query Match          3.2%; Score 7; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 96 SSLSSAS 102  
Db 68 SSLSSAS 74

## RESULT 12

E64375  
hypothetical protein MJ0605 - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: E64375  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A:Reference numbers: A64300; UID:96337999; PMID:8688087  
A:Accession: E64375  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-134 <BUL>  
A:Cross-references: UNIPROT:Q58022; GB:U67508; GB:L77117; NID:G1591300; PIDN:AA898599.1;  
C:Genetics:  
A:Map position: REV535846-535442  
A:Start codon: GTG

```
Query Match          3.2%; Score 7; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 53 KNLNPKK 59  
|||||  
Db 58 KNLNPKK 64

## RESULT 13

JE0264 cyclin I - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: JE0264  
R;Zhu, X.; Naz, R.K.  
Biochem. Biophys. Res. Commun. 249, 56-60, 1998  
A;Title: Expressin of a novel isoform of cyclin I in human testis.  
A;Reference number: JE0264; MUID:98381026; PMID:9705831  
A;Accession: JE0264  
A;Molecule type: mRNA  
A;Residues: 1-178 <ZHU>  
A;Cross-references: UNIPROT:Q14094  
C;Comment: This protein may have a physiological role in spermatogenesis and/or human st

Query Match 3.2%; Score 7; DB 2; Length 178;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 FALASSL 98  
| | | | |  
Db 66 FALASSL 72

RESULT 14

T49611  
hypothetical protein B3E4\_240 [imported] - *Neurospora crassa*  
C:Species: *Neurospora crassa*  
C:date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C:accession: T49611

R.;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nuss, G.  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: Z25022

A:Reference number: 225022  
A:Accession: T49611  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-185 <SCH>  
A:Cross-references: UNIPROT:Q9P5V8; EMBL:AL35531; GSPDB:GN00116; NCSP:B3E4.240  
A:Experimental source: BAC clone B3E4; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B3E4.240  
A:Map position: 6

Query Match	3.2%	Score 7;	DB 2;	Length 185;
Best Local Similarity	100.0%;	Pred. No. 24;		
Matches	7;	Conservative	0;	Mismatches
			0;	Indels
			0;	Caps
			0;	

Qy 97 SLSSASA 103  
p<sub>b</sub> 34 SLSSASA 40

RESULT 15

T52450  
Ribosomal protein S9 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004  
C/Accession: T52450  
R/Arimura, S.; Takusagawa, S.; Hatano, S.; Nakazono, M.; Hirai, A.; Tautsami, N.  
FEBS Lett. 450, 231-234, 1999  
A/Title: A novel plant nuclear gene encoding chloroplast ribosomal protein S9 ha  
A/Reference number: Z26079  
A/Accession: T52450  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-208 <ARI>  
A/Cross-references: UNIPROT:Q9XJ27; EMBL:AB022676; PIDN:BAAB2396.1  
C/Genetics:  
A/Gen: rps9  
C/Superfamily: ribosomal protein S9/S16

Query Match	3.2%;	Score 7;	DB 2;	Length 208;
Best Local Similarity	100.0%;	Pred. No. 26;		
Matches	7;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	

Qy 94 LASSLS 100  
db 7 LASSLS 13

Search completed: October 13, 2005, 18:55:46  
Job time : 37 secs